

Result No.	Score	Query %			DB	ID	Description
		Match	Length	Length			
1	78.5	12.9	332	2	T04484	probable chitinase	
2	76.5	12.6	245	2	AD0753	flagellar biosynth	
3	76.5	12.6	245	2	S78698	probable export pr	
4	75.5	12.4	436	2	B70939	hypothetical prote	
5	75.5	12.4	519	2	B87353	hypothetical prote	
6	75.5	12.4	635	2	T20910	hypothetical prote	
7	74	12.2	768	2	T22758	hypothetical prote	
8	73.5	12.1	261	2	G65099	probable pyruvate	
9	73.5	12.1	346	2	D75303	conserved hypother	
10	73	12.0	227	2	T04420	ribonuclease (EC 3	
11	72	11.8	175	2	T36798	probable transcrip	
12	72	11.8	2871	2	A55624	fibrillin-1 precur	
13	70.5	11.6	467	2	E95850	probable amino aci	
14	70.5	11.6	587	2	C70893	hypothetical prote	
15	70	11.5	558	2	I58545	glycan precursor	
16	69.5	11.4	424	2	D75330	probable beta-lact	
17	69	11.3	324	2	JC2395	Fas antigen precu	
18	69	11.3	480	2	B61213	hypothetical prote	
19	68.5	11.3	431	1	B63092	conserved hypother	
20	68.5	11.3	484	2	E75138	osmoregulated prol	
21	68	11.2	683	2	T00872	probable protein k	
22	67.5	11.1	384	1	T46966	diheme cytochrome	
23	67.5	11.1	1008	1	GNUVUK	glycoprotein precu	
24	67.5	11.1	1013	2	I50615	receptor-type prot	
25	67	11.0	319	2	JC4390	bovine marrow stroma	
26	67	11.0	332	2	AH3572	oligopeptide trans	
27	67	11.0	394	2	C36942	hypothetical prote	
28	67	11.0	893	2	S51603	receptor-like tyro	
29	67	11.0	898	2	S47489	receptor tyrosine	

A:Residues: 1-245 <PAR>  
A:Cross-references: GB:AL513382; PIDN:CAD05727.1; PID:g1503220; GSPDB:GN00176  
C:Genetics:  
A:Gene: STY2187  
F:Superfamily: flagellar biosynthetic protein flip

```

Query Match      12.6%; Score 76.5; DB 2; Length 245;
Best Local Similarity 30.8%; Pred.No. 4.1;
Matches .33; Conservative          9; Mismatches 38; Indels 27; Gaps 6;

QY      6 LRRLRLVLGLWLALLRSVAGQAPG--TAP-CSRGSWSADLDKCMDCASCRRP---59
        ||||| : ||||| : ||||| : ||||| : ||||| :
Db       1 MRRLLEFLSLAGLW--IFSPAAAQLPGLISQPLAGGGQSLSVTILFTITLTFFLPAIL58

QY      60 --HSDF-----CLGC AAA PPFRL LWP ILG GAL ST FVL   92
        : : : : : : : : : : : : : : : : : : : : : :
Db       59 LMWTSPRTIIVFLGNALGTSPAPNOV-----LLGLALFTTFII 100
        : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 3  
S78698 probable export protein flip precursor - Salmonella typhimurium  
C:Species: Salmonella typhimurium  
C:Date: 01-Feb-1999 #sequence\_revision 01-Feb-1999 #text\_change 09-Jul-2004  
C:Accession: S78698  
R:Onnishi, K.; Fan, F.; Schoenhals, G.J.; Kihara, M.; Macnab, R.M.  
J. Bacteriol. 179, 6092-6099, 1997  
A:Title: The FloI, FloP, FloQ, and FloR proteins of Salmonella typhimurium: putative com  
A:Reference number: S78696; MUID:97464436; PMID:9324257

A;Molecule type: DNA  
A;Residues: 1-245 <OHN>  
A;Cross-references: UNIPROT:P54700; EMBL:L49021; NID:g1066860; PIN:AAB81319.1; PID:g1066860  
A;Note: the sequence of residues 42-241 and the corresponding nucleic acid sequence are  
C;Genetics:  
A;Gene: flip  
C;Function:  
A;Description: may be involved in flagellar assembly; may be involved in export of flagellar  
A;Superfamily: flagellar biosynthetic protein flip  
C;Keywords: flagellum; transmembrane protein  
F;1-21/Domain: signal sequence #status predicted <SIG>  
F;22-245/Product: probable export protein flip #status predicted <WAT>  
F;45-61/Domain: transmembrane #status predicted <TM1>  
F;67-105/Domain: transmembrane #status predicted <TM2>  
F;106-205/Domain: transmembrane #status predicted <TM3>  
F;212-228/Domain: transmembrane #status predicted <TM4>

RESULT 4  
E70939  
hypothetical protein Rv0246 - Mycobacterium tuberculosis (strain H37RV)  
C/Species: Mycobacterium tuberculosis  
C/Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 09-Jul-2004  
C/Accession: E70939  
R/Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Cole, S.T.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Connor, R.; Davies, R.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Rajandream, M.A.; M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998  
A/Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
A/Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A/Reference number: A70500. MUID: 98295987. PMID: 9634230

A:Accession: B70939  
A:Status: preliminary;  
A:Molecule type: DNA  
A:Residues: 1-436 <COL>  
A:Cross-references: UNIPROT:053668; GB:AL021929; GB:AL123456; NID:93242291; PID:  
A:Experimental source: strain H39rv  
C:Genetics:  
A:Gene: RV0246

```

Query Match      12.4%; Score 75.5; DB 2; Length 436;
Best Local Similarity 23.0%; Pred. No. 8;
Matches 35; Conservative 16; Mismatches 52; Indels 49; Gaps 5;

QY      1  MARGSLRRLLRLVLVLGLWALLERSVAGEOA--PGTAPCSRGS--WSADLDKCMDCASCR 56
          | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      142  MPSGTARARILLTEVGVGGAAALTAVVAATLSFVDPQPLSRNIHLMTAAVAMASRAICR 201
          | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY      57  ARPHSDFCLGCAAPAPFRLILW-----PIIGG----- 84
          | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      202  ALPHR--IVPRVHAAGLHLVYVGWTAITNGWYRLLVQLVFGSVILGSSFHSIRVA 259
          | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

QY      85  -----ALSLTFVLGLSGFLVWRRCR 105
          | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      260  AVEGDOPDEKVAWVLFVCVGLLGGIATLWNRVR 291
          | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

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RESULT 5
B87353
hypothetical protein CC0837 [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: B87353

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Query Match	12.4%;	Score	75.5;	DB	2;	Length	519;
Best Local Similarity	24.1%;	Pred. No.	9.1;				
Matches	33;	Conservative	22;	Mismatches	51;	Indels	31;
Gaps							
Qy	9	LLRLVLGLWALLRS-VAGEQAPGTPACSRGS-----SWSADLDKCMD	51				
Db	250	LLILMAITGLGLFUPAAQVLGKGFADAAAATQGAETRKAAGPVCAPFAAGAFQATLRKELR	309				
Qy	52	CASCRARPHSDFCIGCAAAAPAPPRLL-----WPILGALSILTFVLGILLSGLFVWRR	103				
Db	310	LVSDDAALLSQVLRVLRYMYPIAFVYMRGAESLPAAWLAGPAAAVTFLAGVAGSLIWT	369				
Qy	104	CRRRS-----SPPPX	114				
		:	:	:	:	:	:
Db	370	VSADTDPDLIAISPTPM	386				

RESULT 6  
T20910  
hypothetical protein ZK1010.9 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T20910; T27646  
R:McMurray, A.  
submitted to the EMBL Data Library, November 1996  
A:Reference number: Z19345  
A:Accession: T20910

A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-635 <WIL>  
A:Cross-references: UNIPROT:O18288; EMBL:Z81503; PIDN:CAB04115.1; GSPDB:GN00021; CESP:ZK1010.9  
A:Experimental source: clone F14F7  
R.Gardner, A.  
submitted to the EMBL Data Library, November 1996  
A:Reference number: Z20398  
A:Accession: T27646  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-635 <WIL>  
A:Cross-references: EMBL:Z82083; PIDN:CAB04975.1; GSPDB:GN00021; CESP:ZK1010.9  
A:Experimental source: clone ZK1010  
C:Genetics:  
A:Gene: CESP:ZK1010.9  
A:Map position: 3  
A:Introns: 71/3, 184/2, 316/3, 403/1, 444/3, 547/3, 577/3  
C:Superfamily: gamma-aminobutyric acid transporter

Query Match 12.4%; Score 75.5; DB 2; Length 635;  
Best Local Similarity 36.6%; Pred. No. 11;  
Matches 26; Conservative 10; Mismatches 28; Indels 7; Gaps 3;  
QY 31 PGTAPCSRGSSWADLCKMDCASCRRP--HSDFCLG--CAAAPAPFRLLPILGGAL 86  
DB 92 PTTAYKNGGLSP---LIAVVGILFAVPAIHMEFALGQYAAKSPFAAFRRMPLIEGVG 148  
QY 87 SLTFVLGLLSG 97  
DB 149 WMTCLVGAIG 159

RESULT 7  
T22758  
hypothetical protein F55H12.1 - *Caenorhabditis elegans*  
C:Species: *Caenorhabditis elegans*  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T22758  
R.Dobson, R.  
submitted to the EMBL Data Library, October 1996  
A:Reference number: Z19610  
A:Accession: T22758  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-768 <WIL>  
A:Cross-references: UNIPROT:P90890; EMBL:Z81091; PIDN:CAB03142.1; GSPDB:GN00019; CESP:F55H12  
A:Experimental source: clone F55H12  
C:Genetics:  
A:Gene: CESP:F55H12.1  
A:Map position: 1  
A:Introns: 114/3, 189/1, 301/2, 426/3, 513/1, 554/3, 657/3, 687/3, 741/1  
C:Superfamily: gamma-aminobutyric acid transporter

Query Match 12.2%; Score 74; DB 2; Length 769;  
Best Local Similarity 40.0%; Pred. No. 17;  
Matches 20; Conservative 7; Mismatches 19; Indels 4; Gaps 2;  
QY 52 CASCRARP--HSDFCLG--CAAAPAPFRLLPILGGALSLTFVLGLLSG 97  
DB 153 CAFVFAVPAIHMEFALGQYAAKSPFAVFRIMPALGEGVGMWMTCTIVGAVIG 202

RESULT 8  
G69099  
probable pyruvate synthase (EC 1.2.7.1) gamma chain - *Methanobacterium thermoautotrophicum*  
C:Species: *Methanobacterium thermoautotrophicum*  
C:Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 05-May-2000  
C:Accession: G69099  
R.Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwnani, N.; Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.  
J. Bacteriol. 179, 7135-7155, 1997

A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-261 <MTH>  
A:Cross-references: GB:AE000929; GB:AE000666; NID:G2622853; PIDN:AAB86210.1; PID:G262282  
A:Experimental source: strain Delta H  
C:Genetics:  
A:Gene: MTH1740  
C:Superfamily: pyruvate synthase gamma chain  
C:Keywords: coenzyme A; oxidoreductase

Query Match 12.1%; Score 73.5; DB 2; Length 261;  
Best Local Similarity 29.2%; Pred. No. 8.2;  
Matches 19; Conservative 8; Mismatches 21; Indels 17; Gaps 4;  
QY 31 PGTAPCSRGSSWSA-----DLCKMDCASCRA-----RPHS---DFCLGCA-AAAPPA 73  
DB 191 PGSTVKNKTGSRWTFKPVLDKDKCIDCDNCILFCPEGCINREHEIDYDYCKGCGICABKC 250  
QY 74 PFRL 78  
DB 251 PVKAI 255

RESULT 9  
D75303  
conserved hypothetical protein - *Deinococcus radiodurans* (strain R1)  
C:Species: *Deinococcus radiodurans*  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C:Accession: D75303  
R.White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.  
Science 286, 1571-1577, 1999  
A:Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.  
A:Reference number: A75250; MUID:20036896; PMID:10567266  
A:Accession: D75303  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-346 <WHI>  
A:Cross-references: UNIPROT:Q9RSC0; GB:AE002053; GB:AE000513; NID:G6459999; PIDN:AAF1175  
A:Experimental source: strain R1  
C:Genetics:  
A:Gene: DR2205  
A:Map position: 1

Query Match 12.1%; Score 73.5; DB 2; Length 346;  
Best Local Similarity 28.6%; Pred. No. 10;  
Matches 32; Conservative 11; Mismatches 52; Indels 17; Gaps 5;  
QY 12 LLVLGLMLALRSVAGEQAPGTAPCSRGSSWSADLCKMDCASC---RAPHSD----FC 64  
DB 87 LLVTCVGLGVL--TAGSASPWT-----MMVGVALVAFGAVLATVWHLRPAAGSLFFVFA 138  
QY 65 LGCAAA--PPAPFRLLPILGGALSLTFVLGLLSGLVWRRCRRSSPPPX 114  
DB 139 VGTGALPHAPLPALPLALAVSGAAALSVLALGALGANHSTRARPHLAAPP 190

RESULT 10  
T04420  
ribonuclease (EC 3.1.-.-) - barley  
C:Species: *Hordeum vulgare* (barley)  
C:Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
C:Accession: T04420  
R.Rogers, J.C.; Rogers, S.W.  
submitted to the EMBL Data Library, April 1997  
A:Reference number: Z15355  
A:Accession: T04420  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA

A;Residues: 1-227 <ROG>  
A;Cross-references: UNIPROT:O04393; EMBL:AF000940; NID:g2150001; PIDN:AAB58719.1; PID:g2150001  
A;Experimental source: cv. Igri  
C;Genetics:  
A;Introns: 35/3; 87/3  
C;Superfamily: Enterobacter ribonuclease  
C;Keywords: hydrolase

Query Match 12.0%; Score 73; DB 2; Length 227;  
Best Local Similarity 30.0%; Pred. No. 8.2;  
Matches 30; Conservative 11; Mismatches 45; Indels 14; Gaps 4;

QY 21 LLRSVAGQAGTAPCSRG-SSWADLDKMDGACSCARPHSDFCIGCAAPPPAPPLLLW 79  
DB 91 LLSSLRAEWPTLACFASDGLQFNAHEWEKHCTCAQNLFHEGYF---QTAAPPPAPPLLD 147

QY 80 PIL-----GGALSLETVLGLL---SGFLVWRRCRRERS 109  
DB 148 ALASAGVAPDGGYVYLSAVKAIQQGTGFEPFVECNRDES 187

RESULT 11  
T36798  
Probable transcription regulator soxR-like - Streptomyces coelicolor  
C;Species: Streptomyces coelicolor  
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
R;Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
submitted to the EMBL Data Library, July 1999  
A;Reference number: Z21614  
A;Accession: T36798  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-175 <OLI>  
A;Cross-references: UNIPROT:Q9S255; EMBL:AL096811; PIDN:CAB46795.1; GSPDB:GN00070; SCOEI  
A;Experimental source: strain A3(2)  
C;Genetics:  
A;Gene: SCOEI:SC130A.18C

Query Match 11.8%; Score 72; DB 2; Length 175;  
Best Local Similarity 27.3%; Pred. No. 8.4;  
Matches 36; Conservative 13; Mismatches 47; Indels 36; Gaps 6;

QY 2 ARGSLRRLRLIV---LGLWIALRSVAGEQAPGTAP-----CSRGSSWSADLDKMDCA 53  
DB 49 ARDALRRVAFVAAQVRVGIPLATIREALAEPEGTPTEDDWARLSEWSRSELDRIKQL 108

QY 54 SCRAPPHSDFCIGCAAPPPAPPLLLPILGALS-TEVL-----GLLSGFLVWR 102  
DB 109 N-RLRDHLTDCLGC-----GCLSLCTCVLGNPDPAFGERSAGSLIVER 151

QY 103 RCRRRSSPPFX 114  
DB 152 RGSTARGGRAPS 163

RESULT 12  
A55624  
fibrillin-1 precursor - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 23-Mar-1995 #sequence\_revision 23-Mar-1995 #text\_change 09-Jul-2004  
C;Accession: A55624  
R;Yin, W.; Smiley, E.; Germiller, J.; Sanguinetti, C.; Lawton, T.; Pereira, L.; Ramirez, J. Biol. Chem. 270, 1798-1806, 1995  
A;Title: Primary structure and developmental expression of Fbn-1, the mouse fibrillin gene  
A;Reference number: A55624; MUID:95130561; PMID:7829516  
A;Accession: A55624  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-2871 <YIN>  
A;Cross-references: UNIPROT:Q61554; GB:I29454; NID:g575509; PIDN:AAAS56840.1; PID:g575510  
C;Genetics:  
A;Gene: Fbn-1

C;Superfamily: fibrillin; EGF homology  
F;I201-I236/Domain: EGF homology <EGF>

Query Match 11.8%; Score 72; DB 2; Length 2871;  
Best Local Similarity 25.3%; Pred. No. 75;  
Matches 20; Conservative 7; Mismatches 24; Indels 28; Gaps 2;

QY 36' CSRGSSWSADLDKMD-----CASCARPHS-----DFCLGC 67  
DB 2040 CPFGFSWSSRRRCQDLRMSYCYAKFEGGKSSPKSRNHSKQCCALKGEGWGPCELC 2099  
QY 68 AAAPPAPPPRLWPILGGAL 86  
DB 2100 PTEPDEAFRCQCPFGSGII 2118

## RESULT 13

E95850  
Probable amino acid carrier protein [imported] - Sinorhizobium meliloti (strain 1021) ma  
C;Species: Sinorhizobium meliloti  
C;Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 09-Jul-2004  
C;Accession: E95850  
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan  
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001  
A;Title: The complete sequence of the 1.683-kb pSymB megaplasmid from the N2-fixing endo  
A;Reference number: A95842; MUID:21396508; PMID:11481431  
A;Accession: E95850  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-467 <KUR>  
A;Cross-references: UNIPROT:Q92X93; GB:AL591985; PIDN:CAC48469.1; PID:g15139941; GSPDB:G  
A;Experimental source: strain 1021, megaplasmid pSYMB  
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,  
Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;  
L.; Hyman, R.W.; Jones, T.  
Science 293, 668-672, 2001  
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,  
hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.  
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.  
A;Reference number: A96039; MUID:21368234; PMID:11474104  
A;Contents: annotation  
C;Genetics:  
A;Gene: SMB20069  
A;Genome: plasmid  
C;Superfamily: sodium-dependent D-alanine/glycine transport protein

Query Match 11.6%; Score 70.5; DB 2; Length 467;  
Best Local Similarity 26.4%; Pred. No. 25;  
Matches 28; Conservative 14; Mismatches 21; Indels 43; Gaps 7;

QY 10 LRLVLGLWL-----ALLRSVAGROA-PGTAPCSRGs-----SWSADLD 47  
DB 322 LAIMVSGWASGETGAVLSAAFEALPG-----YGNLYVTISALFAFTILGWAYAE 376  
QY 48 KMDSCASCARPHSDFCIGCAAPPPAPPLLLWPI---LGGALSFP 90  
DB 377 KCV-----EYLIGTASA--IPFRIVTWTVAFFGATLSLDF 409

## RESULT 14

C70893  
hypothetical protein Rv1069c - Mycobacterium tuberculosis (strain H37RV)  
C;Species: Mycobacterium tuberculosis  
C;Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 16-Aug-2004  
C;Accession: C70893  
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.  
Cole, S.T.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.;  
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.  
Nature 393, 537-544, 1998  
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A;Reference number: A70500; MUID:98295987; PMID:9634230  
A;Accession: C70893



Job time : 40 secs

A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-587 <COL>  
A:Cross-references: UNIPROT:O53417; GB:AL021897; GB:AL123456; NID:g3256022; PIDN:CAA1718  
A:Experimental source: strain H37Rv  
C:Genetics:  
A:Gene: Rv1069c  
C:Superfamily: Membrane protein

Query Match 11.6%; Score 70.5; DB 2; Length 587;  
Best Local Similarity 32.1%; Pred. No. 30;  
Matches 27; Conservative 3; Mismatches 17; Indels 37; Gaps 5;  
QY 68 AAAP-----PAPRLLPPI-----LGGALSLTFV-----LGLLSG----- 97  
DB 27 AATPQTPEPQPIRSTWIRHYTFTGTAMGLVFWFSMTPLSLPGPLFQGLVSGICGAPG 86  
QY 98 -----FLVW--RRCRRERSPPPX 114  
DB 87 YGLGVFAVNLVRYMRSHNSPPPP 110

## RESULT 15

I56545  
glypican precursor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 26-Jul-1996 #sequence revision 26-Jul-1996 #text\_change 09-Jul-2004  
C:Accession: I56545; JCI1281; PC1132  
R:Litwack, E.D.; Stipp, C.S.; Kumbasar, A.; Lander, A.D.  
J. Neurosci. 14, 3713-3724, 1994  
A:Title: Neuronal expression of glypican, a cell-surface glycosylphosphatidylinositol-an  
A:Reference number: I56545; MUID:94267529; PMID:8207484  
A:Accession: I56545  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-558 <RES>  
A:Cross-references: UNIPROT:P35053; GB:IL34067; NID:G506416; PIDN:AAA41251.1; PID:G506417  
R:Karthikeyan, L.; Maurel, P.; Rauch, U.; Margolis, R.K.; Margolis, R.U.  
Biochem. Biophys. Res. Commun. 188, 395-401, 1992  
A:Title: Cloning of a major heparan sulfate proteoglycan from brain and identification a  
A:Reference number: JCI1281; MUID:93038690; PMID:1417860  
A:Accession: JCI1281  
A:Molecule type: mRNA  
A:Residues: 1-20,'T','22-311,'Y',313-361,'A',363-514,'I',516-558 <KAR>  
A:Cross-references: GB:L02896; NID:g204424; PIDN:AAA86439.1; PID:g204425  
A:Experimental source: brain  
A:Accession: PC1132  
A:Molecule type: protein  
A:Residues: 24-55;424-445 <KA2>  
C:Superfamily: glypican  
C:Keywords: blocked carboxyl end; chondroitin sulfate proteoglycan; glycoprotein; hepara  
P:1-23/Domain: signal sequence #status predicted <SIG>  
P:24-530/Product: glypican #status predicted <MAP>  
F:531-558/Domain: carboxyl-terminal propeptide #status predicted <CTP>  
F:55,486,488,490/Binding site: heparan sulfate (Ser) (covalent) #status predicted  
F:79,116/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:399,512/Binding site: carbohydrate (Thr) (covalent) #status predicted  
F:530/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Ser) (in mature form

Query Match 11.5%; Score 70; DB 2; Length 558;  
Best Local Similarity 37.7%; Pred. No. 32;  
Matches 26; Conservative 6; Mismatches 19; Indels 18; Gaps 5;

QY 11 RLLVLGLWLA--LLRSVAGEQAGTAPCRGSSNSADLDKMDGACR---ARPHSDFC 64  
DB 221 RSFVQGLGVASDVVRKVA--QVFLAPECSRA-----VMKLVYCAHCRGVFGARPCPDYC 272  
QY 65 ----LGCAA 69  
DB 273 RNVLKGCLA 281

Search completed: February 14, 2005, 06:47:35

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 14, 2005, 06:17:38 ; Search time 176 Seconds

(without alignments)  
331.688 Million cell updates/sec

Title: US-10-062-831-59

Perfect score: 608

Sequence: 1 MARGSLRLRLVGLWLA.....LSGFLVRRRRSSPPXP 114

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt\_03.\*

1: uniprot\_spot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	572	94.1	129	1 FN14 HUMAN	Q9np84 homo sapien
2	454	74.7	129	2 Q80XX9	Q80xx9 rattus norv
3	446	73.4	129	1 FN14 MOUSE	Q9cr75 m tumor nec
4	211	34.7	191	2 Q62Q04	Q62q04 homo sapien
5	136.5	22.5	120	2 Q6SIX7	Q6six7 xenopus lae
6	93.5	15.4	285	2 Q72JG0	Q72jg0 thermus the
7	90	14.8	952	2 Q62TA9	Q62ta9 homo sapien
8	88	14.5	184	1 T13C HUMAN	Q96rj3 homo sapien
9	87	14.3	333	2 Q9BZG3	Q9bzg3 homo sapien
10	87	14.3	426	2 Q9BZG2	Q9bzg2 homo sapien
11	85.5	14.1	328	2 Q76B98	Q76b98 xenopus lae
12	84.5	13.9	610	2 Q943G8	Q943g8 oryza sativ
13	80.5	13.2	377	2 Q76DQ0	Q76dq0 neurospora
14	79.5	13.1	377	2 Q82N80	Q82n80 streptomyces
15	79	13.0	341	2 Q9N0B3	Q9n0b3 macaca fasc
16	78.5	12.9	219	2 Q8BM15	Q8bmi5 mus musculus
17	78.5	12.9	332	2 Q42839	Q42839 hordeum vul
18	78.5	12.9	387	2 Q8VD70	Q8vd70 mus musculus
19	78.5	12.9	598	2 Q8P6N1	Q8p6n1 mus musculus
20	78.5	12.9	1208	2 Q8QYTA8	Q8qyta8 mus musculus
21	78	12.8	416	2 Q6N7T8	Q6n7t8 rhodospheudo
22	78	12.8	448	1 FBLS RAT	Q9wvht rattus norv
23	77	12.7	291	2 Q749U7	Q749u7 geobacter s
24	77	12.7	448	1 FBLS MOUSE	Q9wvht mus musculus
25	76.5	12.6	178	2 Q748L8	Q748l8 geobacter s
26	76.5	12.6	245	1 FLIP SALTY	P54700 salmonella
27	76.5	12.6	245	2 Q825R3	Q825r3 salmonella
28	76.5	12.6	732	2 Q81ZX4	Q81zx4 streptomyces
29	76	12.5	216	2 Q7NRH8	Q7nrh8 chromobacte
30	76	12.5	293	2 Q6S6K2	Q6s6k2 sus scrofa
31	76	12.5	411	2 Q8CXG1	Q8cxg1 oceanobacill

32	75.5	12.4	222	2 Q9QEE6	Q9qee6 indian citr
33	75.5	12.4	391	2 Q66LN8	Q66ln8 rhodobacter
34	75.5	12.4	396	2 Q67UT0	Q67ut0 oryza sativ
35	75.5	12.4	436	2 Q53668	Q53668 mycobacteri
36	75.5	12.4	436	2 Q7U2G8	Q7u2g8 mycobacteri
37	75.5	12.4	449	2 Q7DA65	Q7da65 mycobacteri
38	75.5	12.4	519	2 Q9A9X4	Q9a9x4 caulobacter
39	75.5	12.4	635	2 O18288	O18288 caenorhabdi
40	75	12.3	370	2 Q96KN9	Q96kn9 homo sapien
41	75	12.3	1180	2 Q6Z3M5	Q6z3m5 oryza sativ
42	74.5	12.3	112	2 Q8ZB85	Q8zb85 oryza sativ
43	74.5	12.3	202	2 Q80MP4	Q80mp4 indian citr
44	74.5	12.3	330	2 Q86OW5	Q86ow5 mus musculu
45	74	12.2	548	1 LGT3_MOUSE	Q8k406 mus musculu

#### ALIGNMENTS

#### RESULT 1

FN14\_HUMAN  
ID FN14\_HUMAN STANDARD; PRT; 129 AA.  
AC Q9NP84; Q9HC50;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member Fn14 precursor  
DE (Fibroblast growth factor-inducible immediate-early response protein  
DE 14) (FGF-inducible 14) (Tweak-receptor) (TweakR).  
GN Name=TNFRSF12A; Synonyms=FN14;  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC TISSUE=Placenta;  
RX MEDLINE=20216634; PubMed=10751351;  
RA Feng S.-L.Y., Guo Y., Factor V.M., Thorgeirsson S.S., Bell D.W.,  
RA Testa J.R., Peifley K.A., Winkles J.A.;  
RT "The Fn14 immediate-early response gene is induced during liver  
RT regeneration and highly expressed in both human and murine  
RT hepatocellular carcinomas";  
RL Am. J. Pathol. 156:1253-1261(2000).  
[2]  
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
RA Tanaka S., Sugimachi K.;  
RT "Human homologue of Fn14";  
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
[3]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC TISSUE=Uterus;  
RX MEDLINE=238257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Groumwood J., Schmutz J., Myers R.M.,  
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RP FUNCTION.  
RA MEDLINE=21585797; PubMed=11728344; DOI=10.1016/S1074-7613(01)00232-1;  
RX Wiley S.R., Cassiano L., Lofton T., Davis-Smith T., Winkles J.A.,  
RA Lindner V., Liu H., Daniel T.O., Smith C.A., Fanelow W.C.;  
RT "A novel TNF receptor family member binds TNFAIP3 and is implicated in  
RT angiogenesis";  
RL Immunity 15:837-846(2001).  
CC -!- FUNCTION: Receptor for TNFSF12/TWEAK. Weak inducer of apoptosis in  
CC some cell types. Promotes angiogenesis and the proliferation of  
CC endothelial cells. May modulate cellular adhesion to matrix  
CC proteins.  
CC -!- SUBUNIT: Associates with TRAF1 and TRAF2, and probably also with  
CC TRAF3.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=1;  
CC IsoId=Q9NP84-1; Sequence=Displayed;  
CC Name=2;  
CC IsoId=Q9NP84-2; Sequence=VSP\_006519;  
CC -!- TISSUE SPECIFICITY: Highly expressed in heart, placenta and  
CC kidney. Intermediate expression in lung, skeletal muscle and  
CC pancreas.  
CC -!- INDUCTION: By FGF-1 and phorbol ester.  
CC -!- SIMILARITY: Contains 1 TNFR-Cys repeat.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
DR EMBL; AF191148; AAF69108.1; -  
DR EMBL; AB035480; BAA94792.1; -  
DR EMBL; AB035481; BAB17850.1; -  
DR EMBL; BC002718; AAH02718.1; -  
DR Genbank; HGNC:18152; TNFRSF12A.  
DR H-InvDB; HIX0012751; -  
DR MIM; 605914; -  
DR GO; GO:0006928; P:cell motility; TAS.  
DR GO; GO:0007275; P:development; TAS.  
DR InterPro; IPR001368; TNFR\_C6.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; FALSE NEG.  
DR PROSITE; PS00500; TNFR\_NGFR\_2; FALSE NEG.  
KW Alternative splicing; Angiogenesis; Apoptosis; Cell adhesion;  
KW Receptor; Signal; Transmembrane.  
FT SIGNAL 1 27 Potential.  
FT CHAIN 28 129 Tumor necrosis factor receptor  
FT superfamily member Fnl4.  
FT DOMAIN 28 80 Extracellular (potential).  
FT TRANSMEM 81 101 Potential.  
FT DOMAIN 102 129 Cytoplasmic (potential).  
FT REPEAT 36 67 TNFR-Cys (atypical).  
FT DISULFID 36 49 Potential.  
FT DISULFID 52 67 Potential.  
FT VARSPIC 33 67 Missing (in isoform 2).  
FT FTID=VSP\_006519.  
SQ SEQUENCE 129 AA; 13911 MW; BF3FDFB9C1E1C448 CRC64;  
  
Query Match 94.1%; Score 572; DB 1; Length 129;  
Best Local Similarity 93.9%; Pred. No. 6.1e-47;  
Matches 107; Conservative 1; Mismatches 6; Indels 0; Gaps 0;  
  
QY 1 MARGSLRRLRLVLGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCARPH 60  
Db 1 MARGSLRRLRLVLGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCARPH 60  
  
QY 61 SDFCLGCAAPAPFRLLPILGALSLFTVLGLSGFLVWRCRRERSPPPX 114  
Db 61 SDFCLGCAAPAPFRLLPILGALSLFTVLGLSGFLVWRCRRERSPPXI 114

RESULT 2  
Q80XX9 PRELIMINARY; PRT; 129 AA.  
ID Q80XX9  
AC Q80XX9  
DT 01-JUN-2003 (T-EMBLrel. 24, Created)  
DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)  
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)  
DE Type 1 transmembrane protein FNL4 (Hypothetical protein).  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OC NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Mueller A.M., Giegerich G.;  
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Pituitary gland;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Pituitary gland;  
RA Strausberg R.;  
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY255102; AAP06753.1; -  
DR EMBL; BC060537; AAH60537.1; -  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR InterPro; IPR02212; Fibril-assoc.  
KW Hypothetical protein; Transmembrane.  
SQ SEQUENCE 129 AA; 13616 MW; 57143F979CD7AC77 CRC64;  
  
Query Match 74.7%; Score 454; DB 2; Length 129;  
Best Local Similarity 75.4%; Pred. No. 1.1e-35;  
Matches 86; Conservative 6; Mismatches 22; Indels 0; Gaps 0;  
  
QY 1 MARGSLRRLRLVLGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCARPH 60  
Db 1 MARGSLRRLRLVLGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCARPH 60  
  
QY 61 SDFCLGCAAPAPFRLLPILGALSLFTVLGLSGFLVWRCRRERSPPPX 114  
Db 61 SDFCLGCAAPAPFRLLPILGALSLFTVLGLSGFLVWRCRRERSPPXI 114

RESULT 3  
FNL4 MOUSE  
ID FNL4 MOUSE STANDARD; PRT; 129 AA.  
AC Q9CR75; Q9QZW3;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)

RA	Schmerch A., Schein J.E., Jones S.U.M., Marra M.A.;
RT	"Generation and initial analysis of more than 15,000 full-length human
RL	and mouse cDNA sequences.";
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC	-I- FUNCTION: Receptor for TNFSP12/TWEAK (By similarity). Weak inducer
CC	of apoptosis in some cell types. Promotes angiogenesis and the
CC	proliferation of endothelial cells. May modulate cellular adhesion
CC	to matrix proteins.
CC	-I- SUBUNIT: Associates with TRAF1 and TRAF2, and probably also with
CC	TNFR3 (By similarity).
CC	-I- SUBCELLULAR LOCATION: Type I membrane protein.
CC	-I- TISSUE SPECIFICITY: Highly expressed in fetal heart, intestine,
CC	kidney, liver, lung and skin, and in adult heart and ovary.
CC	-I- INDUCTION: By FGF-1.
CC	-I- SIMILARITY: Contains 1 TNFR-Cys repeat.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation
CC	at the European Bioinformatics Institute. There are no restrictions on its
CC	use by non-profit institutions as long as its content is in no way
CC	modified and this statement is not removed. Usage by and for commercial
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC	or send an email to license@isb-sib.ch).
DR	EMBL; AF156164; AA07982.1; -
DR	EMBL; AK005530; BAB24101.1; -
DR	EMBL; AK005382; BAB23989.1; -
DR	EMBL; BC025860; AAB25860.1; -
DR	MED; MG1:1351484; Thirsf12a.
DR	GO; GO:0001726; C:rufles; IDA.
DR	GO; GO:0005515; F:protein binding; IPI.
DR	GO; GO:0007155; P:cell adhesion; IDA.
DR	GO; GO:0045773; P:positive regulation of axon extension; IDA.
DR	GO; GO:0009331; P:substrate-bound cell migration, cell attach. . ; IDA.
DR	InterPro; IPRO01368; TNFR_C6.
DR	PROSITE; PS00652; TNFR_NGFR_1; FALSE NEG.
DR	PROSITE; PS00500; TNFR_NGFR_2; FALSE NEG.
KW	Angiogenesis; Apoptosis; Cell adhesion; Receptor; Signal;
KW	Transmembrane.
FT	SIGNAL 1 27 Potential.
FT	CHAIN 28 129 Tumor necrosis factor receptor
FT	DOMAIN 28 80 Extracellular member Fn14.
FT	TRANSMEM 81 101 Potential.
FT	DOMAIN 102 129 Potential.
FT	REPEAT 36 67 Cytoplasmic (Potential).
FT	DISULFID 36 49 TNFR-Cys (atypical).
FT	DISULFID 52 67 Potential.
FT	CONFLICT 3 4 SA -> PG (in Ref. 1).
FT	SEQUENCE 129 AA; 13641 MW; 1665C68B4D9A253 CRC64;
QY	Query Match 73.4%; Score 446; DB 1; Length 129;
Db	Best Local Similarity 73.7%; Pred. No. 6.5e-35;
Db	Matches 84; Conservative 7; Mismatches 23; Indels 0; Gaps 0;
QY	1 MARGSLRLLLVGLVGLVALLRSVAGEAGPTGPCSGSSWSADLDKCMDCASCRRPH 60
Db	1 MASAWPRSLPQLVLVGVLVLRMAAGEAGPTGPCSGSSWSADLDKCMDCASCRRPH 60
QY	61 SDFCLGCAAAPPAPELLLPILGGALSLTVLGLLSGFLVWRRCRRERSPPPK 114
Db	61 SDFCLGCAAPPAPELLLPILGGALSLVIVLVALVSSFLVWRRCRRERFTTI 114
RESULT 4	
Q6P2Q4	PRELIMINARY; PRT; 191 AA.
AC	O6P2Q4
DT	05-JUL-2004 (TEMBLrel. 27, Created)
DT	05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DE	05-JUL-2004 (TEMBLrel. 27, Last annotation update)
DE	Hypothetical protein (Fragment).

```

OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Warr M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RA Strausberg R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC064377; AAH64377.1; -
KW Hypothetical protein.
FT NON_TER
SQ SEQUENCE 191 AA; 20092 MW; 75B166C4B5F0FA01 CRC64;

Query Match 34.7%; Score 211; DB 2; Length 191;
Best Local Similarity 85.1%; Pred. No. 2.5e-12;
Matches 40; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 68 AAAPAPFRLWPIIGGALSITFVLGSLSGFLVWRCRRSSPPX 114
DB 130 AAAPAPFRLWPIIGGALSITFVLGSLSGFLVWRCRRREKFTTPI 176

RESULT 5
Q6SIX7
ID Q6SIX7 PRELIMINARY; PRT; 120 AA.
AC Q6SIX7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Fnl4.
GN Name=Fnl4;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA Brown S.A.N., Winkles J.A.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY458020; AAR21225.1; -
SQ SEQUENCE 120 AA; 13295 MW; F5B5D0BBA3F7B4F CRC64;

Query Match 22.5%; Score 136.5; DB 2; Length 120;
Best Local Similarity 33.0%; Pred. No. 2.1e-05;
Matches 36; Conservative 16; Mismatches 50; Indels 7; Gaps 3;

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QY 7 RRLRLVLGLWLLRLSVAGEQAPGTAPCSRSGSSWSADLDKCMDCASCRARPHSDFLG 66
DB 4 RNLRLTV-PLLLLVSSAASQ-----GECPEGRAYSQDLGCKMEGSCVCKNSEKDFCQN 57
QY 67 CAAPAP-PRLWPIIGGALSITFVLGSLSGFLVWRCRRSSPPX 114
DB 58 CPSKTEQDPFWIWIWIGFSGAGVFLIIVLSLTVLTHCRKSKFTTPI 106

RESULT 6
Q72JG0
ID Q72JG0 PRELIMINARY; PRT; 285 AA.
AC Q72JG0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=TTCO812;
OS Thermus thermophilus (strain HB27 / ATCC BAA-163 / DSM 7039).
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OC Thermus.
OX NCBI_TaxID=262724;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15064768;
RA Henne A., Brueggemann H., Raasch C., Wierzer A., Hartesch T.,
RA Liesegang H., Johann A., Lienard C., Gohl O., Martinez-Arias R.,
RA Jacobi C., Starkuviene V., Schlenczek S., Dencker S., Huber R.,
RA Klenk H.-P., Kramer W., Merkl R., Gottschalk G., Fritz H.-J.;
RT "The genome sequence of the extreme thermophile Thermus
RT thermophilus.";
RL Nat. Biotechnol. 22:547-553(2004).
DR EMBL; AB017303; AAS81158.1; -
DR InterPro; IPR010982; Lambda_like_DNA.
KW Complete proteome.
SQ SEQUENCE 285 AA; 31440 MW; C3C8A7292A7D6C24 CRC64;

Query Match 15.4%; Score 93.5; DB 2; Length 285;
Best Local Similarity 32.5%; Pred. No. 0.58;
Matches 39; Conservative 6; Mismatches 28; Indels 47; Gaps 6;

QY 1 MARGSLRRLRLVL--GLMLALLRSVAGEQAPGTAPCSRSGSSWSADLDKCMDCASCRAR 58
DB 49 LARGYLRYALLGLDPCGLIALYPS-----APSLPP----- 80
QY 59 PHSDFLGCAAPAPFRLWPIIGGALSITFVLGSLSGFLVWRCRR---ERSPPX 114
DB 81 -----PAPPRPRRALWPLW---LALALGLFLVAGFLWPRPEKVELPPPP 127

RESULT 7
Q6ZTA9
ID Q6ZTA9 PRELIMINARY; PRT; 952 AA.
AC Q6ZTA9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein FLJ44823.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cerebellum;
RA Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.,
RA Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsumoto K., Nakamura Y., Sekine M., Kikuchi K., Kanda K., Wagatsuma M.,
RA Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y.,
RA Sugano S., Nagahara K., Masuho Y., Nagai K., Isogai T.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.

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CC -!- SIMILARITY: Contains 8 EGF-like domains.
DR EMBL; AK126775; BAC8684.1; -.
DR GO; GO:0005509; P:calcium ion binding; IEA.
DR GO; GO:0005198; P:structural molecule activity; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR000152; ASX hydroxyl S.
DR InterPro; IPR000985; ConA-like lec_g1.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR001881; EGF Ca.
DR InterPro; IPR001438; EGF II.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001791; Laminin G.
DR InterPro; IPR003129; TSP N.
DR Pfam; PF00008; EGF; 7.
DR Pfam; PF02210; Laminin G 2; 2.
DR PRINTS; PR00010; EGFLOOD.
DR SMART; SM00181; EGF; 8.
DR SMART; SM00179; EGF CA; 5.
DR SMART; SM00282; LamG; 3.
DR PROSITE; PS00010; ASX HYDROXYL; 3.
DR PROSITE; PS00022; EGF 1; UNKNOWN_8.
DR PROSITE; PS01186; EGF 2; 2.
DR PROSITE; PS00026; EGF 3; 8.
DR PROSITE; PS01187; EGF CA; 1.
DR PROSITE; PS00025; LAM_G_DOMAIN; 2.
DR EGF-like domain.
KW EGF-like domain.
SQ SEQUENCE 952 AA; 99727 MW; F90BC8120FCB6D8B CRC64;

Query Match 14.8%; Score 90; DB 2; Length 952;
Best Local Similarity 30.6%; Pred. No. 3.6;
Matches 33; Conservative 14; Mismatches 37; Indels 24; Gaps 6;

QY 22 LRSVAGE--QAPGTAPCSRGSWSADLDKQMDASCRA-----ARHSDFCLGCA 68
DB 830 LEGLAGQRCQVP-TLIPC-----EANPCLNGGTCTRAAGVSEICNARFSGQCEVAK 880

QY 69 AAP-PAPFLWLLPIIGGALS-LTFVLGLSLGVWVRRRCRRSSPPXP 114
DB 881 GLPLPLPPLLEVAVPACACILLGLLGLSLGILAAKRRQSEGTSPS 928

RESULT 8
T13C_HUMAN STANDARD; PRT; 184 AA.
AC Q96R73.
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 13C (B cell-
DE activating factor receptor) (BAFF receptor) (BAFF-R) (BlyS receptor
DE 3).
GN Name=TNFRSF13C; Synonyms=BAFFR, BR3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=B-cell lymphoma;
RX MEDLINE=21442025; PubMed=11509692; DOI=10.1126/science.1061965;
RA Thompson J.S., Bixler S.A., Qian F., Vora K., Scott M.L.,
RA Chachero T.G., Hession C., Schneider P., Sizing I.D., Mullen C.,
RA Strauch K., Zafari M., Benjamin C.D., Teichopp J., Browning J.L.,
RA Ambrose C.;
RT "BAFF-R, a newly identified TNF receptor that specifically interacts
RT with BAFF."
RL Science 293:2108-2111 (2001).
RN [2]
RP FUNCTION.
RX MEDLINE=21475520; PubMed=11591325; DOI=10.1016/S0960-9822(01)00481-X;
RA Yan M., Brady J.R., Chan B., Lee W.P., Heu B., Harless S.M.,
RA Cancro M.P., Grewal I.S., Dixit V.M.;

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RT "Identification of a novel receptor for B lymphocyte stimulator that
RT is mutated in a mouse strain with severe B cell deficiency."
RL Curr. Biol. 11:1547-1552 (2001).
CC -!- FUNCTION: B-cell receptor specific for TNFSF13B/TALL1/BAFF/Blys.
CC Promotes the survival of mature B-cells and the B-cell response.
CC -!- SUBCELLULAR LOCATION: Type III membrane protein (Probable).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q96RJ3-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q96RJ3-2; Sequence=VSP_006505;
CC Note=No experimental confirmation available;
CC -!- TISSUE SPECIFICITY: Highly expressed in spleen and lymph node, and
CC in resting B-cells. Detected at lower levels in activated B-cells,
CC resting CD4+ T-cells, in thymus and peripheral blood leukocytes.
CC -!- SIMILARITY: Contains 1 TNFR-Cys repeat.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF373846; AAK91826.1; -.
DR PDB; 1MPV; NMR; A=23-35.
DR PDB; 1OOE; X-ray; K/L/M/N/O/P/Q/R=16-46.
DR PDB; 1OSX; NMR; A=1-61.
DR Genew; HGNC:17755; TNFRSF13C.
DR MIM; 606269; -.
DR InterPro; IPR001368; TNFR_C6.
DR PROSITE; PS00652; TNFR_NGFR_1; FALSE NEG.
DR PROSITE; PS00500; TNFR_NGFR_2; FALSE NEG.
DR 3D-structure; Alternative splicing; Immune response; Receptor;
DR Signal-anchor; Transmembrane.
KW DOMAIN 1 78
KW TRANSMEM 79 99
FT FT Extracellular (Potential).
FT FT Signal-anchor for type III membrane
FT FT protein (Potential).
FT FT Cytoplasmic (Potential).
FT FT TNFR-Cys (incomplete).
FT FT By similarity.
FT FT By similarity.
FT FT By similarity.
FT FT P -> PA (in isoform 2).
FT FT /FTID=VSP_006505.
SQ SEQUENCE 184 AA; 18863 MW; F2BF98099A27138 CRC64;

Query Match 14.5%; Score 88; DB 1; Length 184;
Best Local Similarity 26.8%; Pred. No. 1.3;
Matches 34; Conservative 12; Mismatches 41; Indels 40; Gaps 6;

QY 23 RSVAGEQAPGTAPCSRGSWSADLDKQMDASCRA-RPHSDFCLGCAAPAPFLWLP- 80
DB 6 RSLGRDAPAPTPCVPACFDLLVRHCVACGLLRTPRKP-----AGASSAPARTALQFQ 60
QY 81 -----ILGGA---LSLTFVLGL-LSGFLVWVRRCR-----E 107
DB 61 ESVGAGAGEAALPLPGLLFGAPALLGLALVLLVGLVSWRRQRRLRGASSAEPDGD 120
QY 108 RSSPPXP 114
DB 121 KDAPEPL 127

RESULT 9
Q9BZG3 ID Q9BZG3 PRELIMINARY; PRT; 333 AA.
AC Q9BZG3;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Acid phosphatase variant 3.

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GN Name=ACPT;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21309073; PubMed=11414767; DOI=10.1006/geno.2001.6556;
RA Yousef G.M., Diamandis M., Jung K., Diamandis E.P.;
RT "Molecular cloning of a novel human acid phosphatase gene (ACPT) that
is highly expressed in the testis.";
RL Genomics 74:385-395(2001).
DR EMBL; AF321918; AAK09396.1; -.
DR HSSP; P15309; 1ND6.
DR GO; GO:0003993; F:acid phosphatase activity; IEA.
DR InterPro; IPR000560; HisAc_phsphtse.
DR Pfam; PF00328; Acid_phosphat_A; 1.
DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN 1.
SQ SEQUENCE 333 AA; 35402 MW; 0C0237096567B30F CRC64;

Query Match 14.3%; Score 87; DB 2; Length 333;
Best Local Similarity 35.3%; Pred. No. 2.8;
Matches 30; Conservative 6; Mismatches 35; Indels 14; Gaps 5;

QY 31 PG-TAPCSRGSSWSADLCKMDCASCARPHSDFLGCG--AAAPAPFRLIWPILGGALS 87
DB 258 PGCPAPCLGRFYQL-----TAPAPPAHGVSCHGYEAIAPPAP---VVPILLAGAVA 307

QY 88 LTFVLGLSLGFLVWR-RCRRRSSP 111
DB 308 VLVALSLGLGLLAWRPGCLRALGGP 332

RESULT 10
QYBZG2 PRELIMINARY; PRT; 426 AA.
AC QYBZG2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Acid phosphatase.
GN Name=ACPT;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21309073; PubMed=11414767; DOI=10.1006/geno.2001.6556;
RA Yousef G.M., Diamandis M., Jung K., Diamandis E.P.;
RT "Molecular cloning of a novel human acid phosphatase gene (ACPT) that
is highly expressed in the testis.";
RL Genomics 74:385-395(2001).
DR EMBL; AF321918; AAK09393.1; -.
DR HSSP; P15309; 1ND5.
DR GO; GO:0003993; F:acid phosphatase activity; IEA.
DR InterPro; IPR000560; HisAc_phsphtse.
DR Pfam; PF00328; Acid_phosphat_A; 1.
DR PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; UNKNOWN 1.
SQ SEQUENCE 426 AA; 46089 MW; BE930398041DB061 CRC64;

Query Match 14.3%; Score 87; DB 2; Length 426;
Best Local Similarity 35.3%; Pred. No. 3.5;
Matches 30; Conservative 6; Mismatches 35; Indels 14; Gaps 5;

QY 31 PG-TAPCSRGSSWSADLCKMDCASCARPHSDFLGCG--AAAPAPFRLIWPILGGALS 87
DB 351 PGCPAPCLGRFYQL-----TAPAPPAHGVSCHGYEAIAPPAP---VVPILLAGAVA 400

QY 88 LTFVLGLSLGFLVWR-RCRRRSSP 111

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DB 401 VLVALSLGLGLLAWRPGCLRALGGP 425

RESULT 11
QYBZG2 PRELIMINARY; PRT; 328 AA.
AC QYBZG2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Death receptor-M2.
GN Name=XDR-M2;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14668340; DOI=10.1074/jbc.M306217200;
RA Tamura K., Noyama T., Ishizawa Y., Takamatsu N., Shiba T., Ito M.;
RT "Xenopus death receptor-M1 and -M2, new members of the tumor necrosis
factor receptor superfamily, trigger apoptotic signaling by
differential mechanisms.";
RL J. Biol. Chem. 279:7629-7635(2004).
DR EMBL; AB111447; BAD11771.1; -.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001450; 4Fe4S-ferredoxin.
DR InterPro; IPR000488; Death.
DR InterPro; IPR011029; DEATH like.
DR InterPro; IPR001368; TNFR_C6.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF00020; TNFR_C6; 1.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00198; 4FE4S_FERREDOXIN; UNKNOWN 1.
DR PROSITE; PS00017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN 1.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 328 AA; 36586 MW; 3FCDLCCAB8533355 CRC64;

Query Match 14.1%; Score 85.5; DB 2; Length 328;
Best Local Similarity 25.4%; Pred. No. 3.8;
Matches 32; Conservative 11; Mismatches 30; Indels 53; Gaps 6;

QY 35 PCSRGSSWS---ADLCKMDCASCAR-----ARPHS-----DFCL 65
DB 72 PCHTGSFSGFTGLDHLDTCLSCRDDQBEVRPCTATQNAECRCRGTGTCPLDHPCEVCL 131
QY 66 GCAAAPAPFRLIWP-----ILGALSITFVLGLLSGF-----LVWRR 103
DB 132 TCTESCPGHELOFPNCSTSDSHCGPAQSGSWIIGVCPILLILLIGLCLCKHLKW-- 189
QY 104 CRERS 109
DB 190 CKDGRS 195

RESULT 12
QYBZG2 PRELIMINARY; PRT; 610 AA.
AC QYBZG2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative receptor protein kinase.
GN Names=P0046E05.12;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Embryophyta; Streptophyta; Tracheophyta;

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OC Spermatozoa; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzae; Oryza.  
 OX NCBI\_TaxID=39947;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX PubMed=12447438; DOI=10.1039/nature01184;  
 RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,  
 RA Wu J., Nilmura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,  
 RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,  
 RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Hayada C.,  
 RA Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,  
 RA Ikono M., Itoh S., Itoh T., Itoh Y., Iwabuchi A., Kamiya K.,  
 RA Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,  
 RA Machita K., Machihara T., Mizuno H., Mizubayashi T., Mukai Y.,  
 RA Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,  
 RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,  
 RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,  
 RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,  
 RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,  
 RA Yano M., Jiang J., Gojobori T.;  
 RT "The genome sequence and structure of rice chromosome 1.";  
 RL Nature 420:312-316(2002).  
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
 DR EMBL; AP003237; BAB67905.1; -;  
 DR Gramene; Q943G8; -;  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR011009; Kinase\_like.  
 DR InterPro; IPR000719; Prot\_Kinase.  
 DR InterPro; IPR008271; Ser\_Thr\_pkin\_AS.  
 DR ProDom; PD000001; Prot\_Kinase; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 KW ATP-binding; Kinase; Receptor; Serine/threonine-protein kinase;  
 KW Transferrase.  
 SQ SEQUENCE 610 AA; 64405 MW; 2A7B3EBE83FA9303 CRC64;  
 Query Match 13.9%; Score 84.5; DB 2; Length 610;  
 Best Local Similarity 24.5%; Pred. No. 8.2;  
 Matches 34; Conservative 13; Mismatches 35; Indels 57; Gaps 4;  
 QY 30 APGTAPCSRGSGWSADLCKMD-----CASCRAPHSDF 63  
 Db 84 SPGDSSTYGGSGSTSTATVSTADPNAGDVPTSGDAIPSSACKPAARCPNRPATD- 142  
 QY 64 CLGCAAPAPFRLLP-----ILGALSITFVLGLSG- 97  
 Db 143 --NVPASPPPPRISLSPPPPPTQSGASSGSKSNGTVVAVGVAAVVLGLAAGL 200  
 QY 98 --FLVWRRCRRSSPPPX 114  
 Db 201 IYFVSKRRRRRQHPPPH 219  
 RESULT 13  
 Q7SD00  
 ID Q7SD00 PRELIMINARY; PRT; 378 AA.  
 AC Q7SD00;  
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Predicted protein (Hypothetical protein B10D6.110).  
 GN Name=NCU02856.1; Synonyms=B10D6.110;  
 OS Neurospora crassa.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.  
 OX NCBI\_TaxID=5141;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=OR74A;

RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,  
 RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,  
 RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,  
 RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,  
 RA Seilrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,  
 RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,  
 RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,  
 RA Kamal M., Kamysvselis M., Mauceli E., Bielke C., Rudd S., Frishman D.,  
 RA Kryofova S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,  
 RA Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A.,  
 RA Desouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,  
 RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,  
 RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,  
 RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.;  
 RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";  
 RL Nature 0:0-0(2003).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,  
 RA Nyakatura G., Mewes H.W., Mannhaupt G.;  
 RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA German Neurospora genome project;  
 RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.  
 CC -1- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL; AABX01000046; EAA34910.1; -;  
 DR EMBL; BX842624; CAE76227.1; -;  
 DR Hypothetical protein.  
 KW SEQUENCE 378 AA; 42342 MW; 1C923B48C2CB6730 CRC64;  
 Query Match 13.2%; Score 80.5; DB 2; Length 378;  
 Best Local Similarity 31.9%; Pred. No. 13;  
 Matches 38; Conservative 11; Mismatches 45; Indels 25; Gaps 7;  
 QY 15 LGLMALILRS---VAGEOAPGTAPC-----SRGSGWSADLCKMDCA-SCRAPHSDFCL 65  
 Db 1 MGLAAPRKSHQVAPQIPDTLPAPSQPQSPQTSYALSSVTETATTSATPLPKL 60  
 QY 66 GCAAPAPFRLLPIL-----GGALSITFVLGLSG-----FLVWRRCRRSSP 111  
 Db 61 LAILKTPTFSF--PVLATSSSAHSAVALGIVGVFGFTIIFSFIWRLCRR-RSTP 116  
 RESULT 14  
 Q82N80  
 ID Q82N80 PRELIMINARY; PRT; 377 AA.  
 AC Q82N80;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 GN OrderedLocusNames=SAV1423;  
 OS Streptomyces avermitilis.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Streptomyces; Streptomycetaceae; Streptomyces.  
 OX NCBI\_TaxID=33903;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MA-4680;  
 RX MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;  
 RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,  
 RA Shinoe M., Takahashi Y., Horikawa H., Nakazawa H., Osone T.,  
 RA Kikuchi H., Shiba T., Sakai Y., Hattori M.;  
 RT "Genome sequence of an industrial microorganism Streptomyces  
 RT avermitilis: deducing the ability of producing secondary  
 RT metabolites.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=MA-4680;



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 14, 2005, 06:15:59 ; Search time 164 Seconds  
(without alignments)  
268.846 Million cell updates/sec

Title: US-10-062-831-59  
Perfect score: 608  
Sequence: 1 MARGSLRLLRLVGLMLA.....LSGLVWRCRRSSPPPX 114

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: Geneseqp1980a:\*  
2: Geneseqp1990a:\*  
3: Geneseqp2000a:\*  
4: Geneseqp2001a:\*  
5: Geneseqp2002a:\*  
6: Geneseqp2003a:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004a:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description.
1	608	100.0	114	2	Aaw73409 Human sec
2	572	94.1	129	2	Aaw88506 Human liv
3	572	94.1	129	3	Aay57940 Human tra
4	572	94.1	129	4	Aau03498 Human TWE
5	572	94.1	129	5	Abp61512 Human NF-
6	572	94.1	129	5	Abp79827 Human typ
7	572	94.1	129	6	Ada56889 Human sec
8	572	94.1	129	6	Abu56716 Lung canc
9	572	94.1	129	7	Adc74112 Human sec
10	572	94.1	129	7	Adc37867 Human sec
11	572	94.1	129	7	Add89033 TAT1274. 1
12	572	94.1	129	7	Abu64232 Human FRA
13	572	94.1	129	7	Adn39126 Cancer/an
14	572	94.1	129	7	Adn39987 Cancer/an
15	572	94.1	129	8	Abm81706 Tumour-as
16	451	74.2	129	5	Aau79828 Mouse typ
17	433	71.2	309	4	Aau03500 Human TWE
18	337.5	55.5	94	7	Abu64233 Human CRY
19	274.5	45.1	112	3	Aay91463 Human sec
20	274.5	45.1	112	6	Ada57390 Human sec
21	274.5	45.1	112	7	Adc74462 Human sec
22	274.5	45.1	112	7	Add38025 Human sec
23	274.5	45.1	112	8	Adl71535 Novel hum
24	274.5	45.1	155	3	Aay91604 Human sec
25	274.5	45.1	155	6	Ada57391 Human sec

ALIGNMENTS

RESULT 1

AAW73409  
ID AAW73409 standard; protein; 114 AA.

XX AC AAW73409;

XX 19-FEB-1999 (first entry)

XX Human secreted protein encoded by Gene No. 13.

XX Secreted protein; human; protein therapy; gene therapy; blood disorder;  
pathological condition; diagnosis; cancer; neurological disorder;  
developmental abnormality; foetal deficiency; leukaemia; hepatic disease;  
immune system disorder; Alzheimer's disease; cognitive disorder;  
schizophrenia; prostate disease; autoimmune disorder; AIDS.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Misc-difference 114 /note= "unspecified amino acid"

XX WO9854206-A1.

XX 03-DEC-1998.

XX 28-MAY-1998; 98WO-US010868.

XX 30-MAY-1997; 97US-0044039P.

XX 30-MAY-1997; 97US-0048093P.

XX 30-MAY-1997; 97US-0048101P.

XX 30-MAY-1997; 97US-0048190P.

XX 30-MAY-1997; 97US-0048356P.

XX 30-MAY-1997; 97US-0050935P.

XX 29-AUG-1997; 97US-0056250P.

XX 29-AUG-1997; 97US-0056293P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM, Rosen CA, Carter KC, Dillon PJ, Endress GA, Yu G;

XX Ni J, Peng P;

XX WPI; 1999-070209/06.

XX N-PSDB; AAV08823.

XX New isolated human genes - useful for diagnosis and treatment of, e.g.  
cancers, neurological disorders, immune diseases, developmental disorders

PT or blood disorders.  
 XX Claim 11; Page 153; 189pp; English.  
 XX This sequence is encoded by a cDNA of the invention, designated Gene No. 13. This sequence represents a human secreted protein, and is expressed in keratinocytes and to a lesser extent in endothelial cells and placenta. The DNA sequences of the invention and their corresponding secreted polypeptides are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the DNA sequences. Specific uses are described for each of the DNA sequences and the encoded proteins, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, neurological disorders, developmental abnormalities and foetal deficiencies, blood disorders, leukaemias, diseases of the immune system (including allergies or asthma), hepatic disease, Alzheimer's and cognitive disorders, schizophrenia, prostate disease, autoimmune disorders and AIDS. The polypeptides are also useful for identifying their binding partners  
 XX Sequence 114 AA;  
 SQ Query Match 100.0%; Score 608; DB 2; Length 114;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-55;  
 Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY .1 MARGSLRLLRLVLLGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCARPH 60  
 Db 1 MARGSLRLLRLVLLGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCARPH 60  
 QY 61 SDFCLGCAAAAPPAPFRLWPILGALSLTFVLGSLGFLVWRCRRERSPPPX 114  
 Db 61 SDFCLGCAAAAPPAPFRLWPILGALSLTFVLGSLGFLVWRCRRERSPPPX 114  
 RESULT 2  
 AAW88506  
 ID AAW88506 standard; protein; 129 AA.  
 AC AAW88506;  
 XX 30-MAR-1999 (first entry)  
 XX Human liver clone HP10432-encoded membrane protein.  
 DE Transmembrane protein; HP10432; human; liver.  
 KW Homo sapiens.  
 OS WO9855508-A2.  
 FN 10-DEC-1998.  
 PD 03-JUN-1998; 98WO-JP002445.  
 PF 03-JUN-1997; 97JP-00144948.  
 PR (SAGA) SAGAMI CHEM RES CENTRE.  
 XX (PROT-) PROTEGENE INC.  
 PA Kato S, Sekine S, Yamaguchi T;  
 PI WPI; 1999-045730/04.  
 DR N-PSDB; AAW84374.  
 XX New human proteins containing transmembrane domains and their encoding sequences - useful in the preparation of antibodies and large-scale protein production, gene diagnosis, and gene therapy.  
 PT Claim 1; Page 152-153; 178pp; English.  
 XX

CC This is the amino acid sequence of a transmembrane protein encoded by human liver cDNA clone HP10432 (see AAW84374). The encoded protein has a signal-like N-terminal region and one internal transmembrane domain. The invention provides nucleotide sequences (see AAW84359-76) coding for 18 transmembrane proteins (see AAW8491-508), vectors containing such polynucleotides, and eukaryotic cells containing the vectors. The proteins can be used as antigens or as compositions in the preparation of antibodies against the proteins. The polynucleotides can be used as probes for gene diagnosis, and as gene sources for gene therapy and large scale production of proteins encoded by the cDNA. The host cells are used for the detection of ligands corresponding to the expressed proteins, and the screening of low mol.wt. medicines  
 XX Sequence 129 AA;  
 SQ Query Match 94.1%; Score 572; DB 2; Length 129;  
 Best Local Similarity 93.9%; Pred. No. 1.6e-51;  
 Matches 107; Conservative 1; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 MARGSLRLLRLVLLGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCARPH 60  
 Db 1 MARGSLRLLRLVLLGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCARPH 60  
 QY 61 SDFCLGCAAAAPPAPFRLWPILGALSLTFVLGSLGFLVWRCRRERSPPPX 114  
 Db 61 SDFCLGCAAAAPPAPFRLWPILGALSLTFVLGSLGFLVWRCRRREKFTTPI 114  
 RESULT 3  
 AAY57940  
 ID AAY57940 standard; protein; 129 AA.  
 AC AAY57940;  
 XX 23-MAR-2000 (first entry)  
 XX Human transmembrane protein HTMPN-64.  
 DE Human; transmembrane protein; HTMPN; diagnosis; immunospecific; antiproliferative; neuroprotective; immune disorder;  
 KW reproductive disorder; smooth muscle disorder; neurological disorder; gastrointestinal disorder; developmental disorder;  
 KW cell proliferative disorder.  
 XX Homo sapiens.  
 OS WO9961471-A2.  
 FN 02-DEC-1999.  
 PD 28-MAY-1999; 99WO-US011904.  
 PF 29-MAY-1998; 98US-0087260P.  
 PR 02-JUL-1998; 98US-0091674P.  
 PR 02-OCT-1998; 98US-0102954P.  
 PR 24-NOV-1998; 98US-0109869P.  
 XX (INCY-) INCYTE PHARM INC.  
 XX Tang YT, Lal P, Hillman JL, Yue H, Guegler KJ, Corley NC;  
 PI Bandman O, Patterson C, Gorgone GA, Kaser MR, Baughn MR, Au-Young J;  
 PI WPI; 2000-072605/06.  
 DR N-PSDB; AAZ56761.  
 XX Proteins, polynucleotides, vectors, host cells and antibodies used to diagnose, treat or prevent immune, reproductive, smooth muscle, neurological, gastrointestinal, developmental and cell proliferative disorders.  
 PT Claim 1; Page 163; 229pp; English.  
 PS AAZ56698 to AAZ56776 encode AAY57877 to AAY57955 which represent human  
 CC



DR WPI; 2002-583617/62.  
DR N-PSDB; ABQ92000.  
XX  
PT NF-approximatelykB activating gene and expressed protein, applicable in  
PT diagnosis and screening inhibitors or promoters to control excessive  
PT activation or inhibition for treating e.g. inflammations, autoimmune  
PT diseases and cancer.  
XX  
PS Claim 4; Page 814-815; 841pp; Japanese.  
XX  
CC The invention relates to a purified protein (I), comprising one of 90  
CC fully defined sequences (ABP61424-ABP61513) or a protein based on any of  
CC the sequences but with some amino acids deleted, substituted or added and  
CC with a NF-kB (nuclear factor kappa B) activating effect. The protein and  
CC encoding gene (ABQ91912-ABQ92001) are useful in diagnosis and screening  
CC inhibitors or promoters to control excessive activation or inhibition and  
CC for treating e.g. inflammations, autoimmune diseases, cancers,  
CC infections, bone diseases, AIDS, neurodegenerative diseases or ischaemic  
CC disorders  
XX  
SQ Sequence 129 AA;  
Query Match 94.1%; Score 572; DB 5; Length 129;  
Best Local Similarity 93.9%; Pred. No. 1.6e-51;  
Matches 107; Conservative 1; Mismatches 6; Indels 0; Gaps 0;  
Qy 1 MARGSLRLRLVGLWLLRLSVAGQAPGTAPCSRGSWSADLCKMDCASCRRPH 60  
Db 1 MARGSLRLRLVGLWLLRLSVAGQAPGTAPCSRGSWSADLCKMDCASCRRPH 60  
Qy 61 SDFCLGCAAAAPPAPFRLWLPILGGLSLTFVLGSLGFLVWRCRRERSPPPX 114  
Db 61 SDFCLGCAAAAPPAPFRLWLPILGGLSLTFVLGSLGFLVWRCRRERSPPPX 114  
RESULT 6  
AAU79827  
ID AAU79827 standard; protein; 129 AA.  
XX  
AC AAU79827;  
XX  
DT 15-JUL-2002 (first entry)  
XX  
DE Human type 1 transmembrane protein Fn14.  
XX  
KW Type 1 transmembrane protein Fn14; human; cytostatic; cardiant;  
KW vulnery; TWEAK agonist; Fn14 agonist; angiogenesis; tumour progression;  
KW tumour necrosis factor family; TNF family; TWEAK receptor;  
KW myocardial ischaemic condition; myocardial infarction; wound healing;  
KW burn healing; gastric ulcer; tissue transplantation;  
KW organ transplantation; neovascularisation; vascular insufficiency;  
KW cancer; inflammatory macular degeneration; diabetic retinopathy.  
XX  
OS Homo sapiens.  
XX  
PN WO200222166-A2.  
XX  
PD 21-MAR-2002.  
XX  
PF 12-SEP-2001; 2001WO-US028451.  
XX  
PR 14-SEP-2000; 2000US-0232355P.  
XX  
PA (BIOJ ) BIOGEN INC.  
XX  
PI Browning J, Burkly L, Jakubowski A, Zheng T;  
XX  
DR WPI; 2002-383103/41.  
XX  
PT Methods of modulating angiogenesis and inhibiting tumor progression,  
PT using TWEAK receptor agonists.  
XX  
PS Disclosure; Fig 10A; 37pp; English.

XX The invention describes methods of modulating angiogenesis and inhibiting  
CC tumour progression using TWEAK (a novel member of the tumour necrosis  
CC factor or TNF family) receptor agonists. Conditions which can be treated  
CC using the agonists include myocardial ischaemic conditions (e.g.  
CC myocardial infarction), wound healing (e.g. burn healing and healing of  
CC gastric ulcers), and tissue and organ transplantations to promote  
CC neovascularisation, particularly in subjects suffering from vascular  
CC insufficiency (e.g. diabetic patients). Inhibition of angiogenesis and  
CC subsequently neovascularisation is useful in treatment of cancer,  
CC inflammatory macular degeneration and diabetic retinopathy. This sequence  
CC represents the human type 1 transmembrane protein Fn14, a TWEAK receptor  
CC described in the invention  
XX  
SQ Sequence 129 AA;  
Query Match 94.1%; Score 572; DB 5; Length 129;  
Best Local Similarity 93.9%; Pred. No. 1.6e-51;  
Matches 107; Conservative 1; Mismatches 6; Indels 0; Gaps 0;  
Qy 1 MARGSLRLRLVGLWLLRLSVAGQAPGTAPCSRGSWSADLCKMDCASCRRPH 60  
Db 1 MARGSLRLRLVGLWLLRLSVAGQAPGTAPCSRGSWSADLCKMDCASCRRPH 60  
Qy 61 SDFCLGCAAAAPPAPFRLWLPILGGLSLTFVLGSLGFLVWRCRRERSPPPX 114  
Db 61 SDFCLGCAAAAPPAPFRLWLPILGGLSLTFVLGSLGFLVWRCRRERSPPPX 114  
RESULT 7  
ADA56889  
ID ADA56889 standard; protein; 129 AA.  
XX  
AC ADA56889;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Human secreted protein #172.  
XX  
KW immunosuppressive; antiinflammatory; antiasthmatic; antiallergic;  
KW cytostatic; cerebroprotective; neuroprotective; nootropic;  
KW cardiovascular; antiarteriosclerotic; gene therapy;  
KW human secreted protein; immune disorder; inflammation;  
KW respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;  
KW inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;  
KW multiple sclerosis; ischaemic brain injury; Parkinson's disease;  
KW Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;  
KW triple helix formation; antisense gene therapy; forensic biology.  
XX  
OS Homo sapiens.  
XX  
PN WO2002102994-A2.  
XX  
PD 27-DEC-2002.  
XX  
PR 19-MAR-2002; 2002WO-US008278.  
XX  
PR 21-MAR-2001; 2001US-0277340P.  
PR 19-JUL-2001; 2001US-0306171P.  
PR 13-NOV-2001; 2001US-0331287P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Rosen CA, Ruben SM;  
XX  
DR WPI; 2003-167512/16.  
DR N-PSDB; ADA55993.  
XX  
PT New human secreted polypeptides and polynucleotides, useful for  
PT diagnosing, treating or preventing e.g. immune disorders, inflammatory  
PT conditions, respiratory disorders, cancers, CNS disorders, or  
PT neurodegenerative disorders.  
XX

PS Claim 13; SEQ ID NO 1079; 1754pp; English.

XX The invention relates to 592 new human secreted polypeptides useful for

CC diagnosing, treating or preventing e.g. immune disorders, inflammatory

CC conditions, respiratory disorders, cancers, CNS disorders, or

CC neurodegenerative disorders, or polypeptides comprising an amino acid

CC sequence at least 95% identical to the new sequences. The polypeptides,

CC antibodies or antibody fragments that bind to the polypeptides, nucleic

CC acids encoding the polypeptides, agonists or antagonists that binds to

CC the polypeptide, are useful in preparing diagnostic or pharmaceutical

CC compositions for diagnosing, treating or preventing an e.g. immune

CC disorders, inflammatory conditions (e.g. inflammatory bowel disease,

CC nephritis or Crohn's disease), respiratory disorders (e.g. asthma and

CC allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders

CC (e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative

CC disorders (e.g. Parkinson's disease or Alzheimer's disease), and

CC cardiovascular disorders (e.g. atherosclerosis or myocarditis). The

CC polynucleotides are useful for chromosome identification, chromosome

CC mapping, for controlling gene expression through triple helix formation

CC or antisense DNA or RNA, in gene therapy, for identifying individuals

CC from minute biological samples, in forensic biology, and as hybridization

CC probes. The polypeptides are useful for as molecular weight markers on

CC sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE)

CC gels, to raise antibodies, for testing biological activities, and for

CC treating or preventing neural disorders, immune system disorders,

CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,

CC renal, proliferative and/or cancerous diseases. This sequence corresponds

CC to one of the polypeptide of the invention. Note: The sequence data for

CC this patent did form part of the printed specification, but was obtained

CC in electronic format directly from WIPO at

CC ftp.wipo.int/pub/published\_pct\_sequences.

XX

SQ Sequence 129 AA;

Query Match 94.1%; Score 572; DB 6; Length 129;

Best Local Similarity 93.9%; Pred. No. 1.6e-51;

Matches 107; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 MARGSLRLRLRLVGLWLLALLRSVAGEQAPCTAPCSRGSSWSADLDKCMDCASCRRAPH 60

DB 1 MARGSLRLRLRLVGLWLLALLRSVAGEQAPCTAPCSRGSSWSADLDKCMDCASCRRAPH 60

QY 61 SDFCLGCAAAAPPAPFRLWLPILGGALSLTFVLGSLGFLVWRCRRRERSPPPX 114

DB 61 SDFCLGCAAAAPPAPFRLWLPILGGALSLTFVLGSLGFLVWRCRRRERSPPX 114

RESULT 8

ABU56716

ID ABU56716 standard; protein; 129 AA.

AC ABU56716;

XX

XX 02-APR-2003 (first entry)

DT

XX

DE Lung cancer-associated polypeptide #309.

XX

XX Lung cancer-associated polypeptide; cytostatic; emphysema;

XX antiinflammatory; antiaesthetic; non-small cell lung cancer; atelectasis;

KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;

KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;

KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.

XX

OS Unidentified.

XX

XX WO200286443-A2.

FN

XX

XX 31-OCT-2002.

PD

XX

XX 18-APR-2002; 2002WO-US012476.

PF

XX

XX 18-APR-2001; 2001US-0284770P.

PR

XX 10-MAY-2001; 2001US-0290492P.

PR 09-NOV-2001; 2001US-0339245P.

PR 13-NOV-2001; 2001US-0350666P.

PR 29-NOV-2001; 2001US-0334370P.

PR 12-APR-2002; 2002US-0372246P.

XX (EOSB-) EOS BIOTECHNOLOGY INC.

XX

XX Aziz N, Murray R;

PI

XX WPI; 2003-093161/08.

DR N-P8DB; ABX76445.

XX

PT Detecting a lung cancer-associated transcript in a cell from a patient

PT for treating lung cancer, by contacting a biological sample from the

PT patient with a polynucleotide that exhibits increased or decreased

PT expression in lung cancer.

XX

PS Claim 27; Page 429; 453pp; English.

XX

CC The invention relates to a method for detecting a lung cancer-associated

CC transcript in a cell from a patient, comprising contacting a biological

CC sample from the patient with a polynucleotide that selectively hybridises

CC to a sequence that is at least 80 % identical to a gene that exhibits

CC increased or decreased expression in lung cancer samples. Lung cancer-

CC associated polynucleotides and polypeptides are used for identifying a

CC compound that modulates a lung cancer-associated polypeptide, for

CC inhibiting proliferation of a lung cancer-associated cell to treat lung

CC cancer in a patient and for treating a mammal having lung cancer by

CC administering a modulatory compound identified. The methods are useful

CC for treating lung cancer, such as small cell lung cancer, non-small cell

CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,

CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,

CC hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and

CC bronchiectasis. The genes, polynucleotides and polypeptides are useful

CC for diagnostic purposes and as targets for screening for therapeutic

CC compounds that modulate lung cancer, such as antibodies. Sequences

CC ABU56408-ABU56745 represent lung cancer-associated polypeptides of the

CC invention

XX

SQ Sequence 129 AA;

Query Match 94.1%; Score 572; DB 6; Length 129;

Best Local Similarity 93.9%; Pred. No. 1.6e-51;

Matches 107; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 MARGSLRLRLRLVGLWLLALLRSVAGEQAPCTAPCSRGSSWSADLDKCMDCASCRRAPH 60

DB 1 MARGSLRLRLRLVGLWLLALLRSVAGEQAPCTAPCSRGSSWSADLDKCMDCASCRRAPH 60

QY 61 SDFCLGCAAAAPPAPFRLWLPILGGALSLTFVLGSLGFLVWRCRRRERSPPPX 114

DB 61 SDFCLGCAAAAPPAPFRLWLPILGGALSLTFVLGSLGFLVWRCRRRERSPPX 114

RESULT 9

ADC74112

ID ADC74112 standard; protein; 129 AA.

XX

XX ADC74112;

AC

XX

XX 01-JAN-2004 (first entry)

DT

XX

XX Human secreted protein - SEQ ID 745.

DE

XX

XX antianaemic; antirheumatic; antiarthritic; antiinflammatory; antithyroid;

KW antidabetic; immunosuppressive; dermatological; nephrotropic;

KW antiparkinsonian; neuroprotective; nootropic; antibacterial; virucide;

KW fungicide; antiparasitic; antiarteriosclerotic; vulnary; cytostatic;

KW haemopoietic; haematologic; anaemia; autoimmune disorder;

KW rheumatoid arthritis; inflammation; Grave's disease; diabetes;

KW systemic lupus erythematosus; glomerulonephritis; neurodegenerative;

KW Parkinson's; Alzheimer's; wound; hyperproliferative; atherosclerosis;

KW cancer; bacterial; viral; fungal; parasitic infection; gene therapy;

KW human.  
XX Homo sapiens.  
OS WO2003038063-A2.  
XX PD 08-MAY-2003.  
XX PF 19-MAR-2002; 2002WO-US008277.  
XX PR 21-MAR-2001; 2001US-0277340P.  
XX PR 19-JUL-2001; 2001US-0306171P.  
XX PR 13-NOV-2001; 2001US-0331287P.  
XX PA (HUMA-) HUMAN GENOME SCI INC.  
XX PI Rosen CA, Ruben SM;  
XX DR WPI; 2003-430516/40.  
XX DR N-PSDB; ADC73497.  
XX PT New human secreted polypeptide for diagnosing, preventing or treating  
XX PT hematopoietic or hematologic disorders (e.g. anemia), autoimmune  
XX PT disorders (e.g. diabetes) or hyperproliferative disorders (e.g. cancer or  
XX PT atherosclerosis).  
XX PS Claim 16; SEQ ID NO 745; 2272pp; English.  
XX PT The invention relates to a novel human secreted polypeptide comprising a  
XX CC defined sequence given in the specification. The polypeptide, nucleic  
XX CC acid molecule, antibody, agonist or antagonist of the invention may be  
XX CC useful for preparing a composition for diagnosing or treating a  
XX CC disease, haemopoietic or haematologic disorder such as anaemia, autoimmune  
XX CC disorders such as rheumatoid arthritis, inflammation, Grave's disease,  
XX CC diabetes, systemic lupus erythematosus or glomerulonephritis,  
XX CC neurodegenerative disorders including Parkinson's disease and Alzheimer's  
XX CC disease, wounds and hyperproliferative disorders including  
XX CC atherosclerosis or cancer, as well as bacterial, viral, fungal or  
XX CC parasitic infections. The polypeptide may also be used during gene  
XX CC therapy procedures and for identifying a binding partner by contacting  
XX CC the polypeptide with a binding partner and determining whether the  
XX CC binding partner increases or decreases the activity of the polypeptide.  
XX CC The current sequence is that of the human secreted protein of the  
XX CC invention.  
XX SQ Sequence 129 AA;  
Query Match 94.1%; Score 572; DB 7; Length 129;  
Best Local Similarity 93.9%; Pred. No. 1.6e-51;  
Matches 107; Conservative 1; Mismatches 6; Indels 0; Gaps 0;  
QY 1 MARGSLRLRLLLVLGLMLALLRSVAGEQAPGTAPCSRGSWSADLCKMDCASCARPH 60  
Db 1 MARGSLRLRLLLVLGLMLALLRSVAGEQAPGTAPCSRGSWSADLCKMDCASCARPH 60  
QY 61 SDFCLGCAAAPAPAPFLLWPILGGALSLTFVLGLSGFLVWRCRRRSPPPX 114  
Db 61 SDFCLGCAAAPAPAPFLLWPILGGALSLTFVLGLSGFLVWRCRRRREKFTTPI 114  
RESULT 10  
ADD37867  
ID ADD37867 standard; protein; 129 AA.  
XX AC ADD37867;  
XX DT 15-JAN-2004 (first entry)  
XX DE Human secreted protein #50.  
XX KW human secreted protein; Antiallergic; Antiinflammatory; Antibacterial;  
XX KW Anti-HIV; Cytostatic; Immunosuppressive; Hemostatic.

OS Homo sapiens.  
XX PN WO200290526-A2.  
XX PD 14-NOV-2002.  
XX PF 19-MAR-2002; 2002WO-US008279.  
XX PR 21-MAR-2001; 2001US-0277340P.  
XX PR 19-JUL-2001; 2001US-0306171P.  
XX PR 13-NOV-2001; 2001US-0331287P.  
XX PA (HUMA-) HUMAN GENOME SCI INC.  
XX PI Rosen CA, Ruben SM;  
XX DR WPI; 2003-140218/13.  
XX PT New human secreted proteins and nucleic acid molecules, useful for  
XX PT preparing a diagnostic or pharmaceutical composition for diagnosing or  
XX PT treating allergic or asthmatic disorders, or related immediate  
XX PT hypersensitivity disorders.  
XX PS Claim 1; SEQ ID NO 349; 1323pp; English.  
XX PT The present invention relates to an isolated polypeptide or human  
XX CC secreted protein. The polypeptides, nucleic acid molecules, antibodies or  
XX CC their fragments, and agonists or antagonists that bind are useful for  
XX CC preparing a diagnostic or pharmaceutical composition for diagnosing or  
XX CC treating allergic or asthmatic disorders. The polypeptide is also useful  
XX CC for identifying a binding partner by contacting the polypeptide with a  
XX CC binding partner, and determining whether the binding partner increases or  
XX CC decreases the activity of the polypeptide. The polypeptides and nucleic  
XX CC acid molecules are also useful for detecting, preventing, diagnosing,  
XX CC prognosticating, treating or ameliorating inflammatory disorders  
XX CC neoplastic diseases, wound healing and disorders of epithelial cell  
XX CC proliferation, immune disorders, cardiovascular disorders, blood-related  
XX CC disorders, infectious diseases, endocrine disorders, or gastrointestinal  
XX CC disorders. The nucleic acids are also useful for chromosome  
XX CC identification, radiation hybrid mapping or long-range restriction  
XX CC mapping, as molecular weight markers, or as hybridization or diagnostic  
XX CC probes. The polypeptides and antibodies are useful for providing  
XX CC immunological probes for differential identification of the tissues  
XX CC immunohistochemistry assays. The present sequence represents a human  
XX CC secreted protein.  
XX SQ Sequence 129 AA;  
Query Match 94.1%; Score 572; DB 7; Length 129;  
Best Local Similarity 93.9%; Pred. No. 1.6e-51;  
Matches 107; Conservative 1; Mismatches 6; Indels 0; Gaps 0;  
QY 1 MARGSLRLRLLLVLGLMLALLRSVAGEQAPGTAPCSRGSWSADLCKMDCASCARPH 60  
Db 1 MARGSLRLRLLLVLGLMLALLRSVAGEQAPGTAPCSRGSWSADLCKMDCASCARPH 60  
QY 61 SDFCLGCAAAPAPAPFLLWPILGGALSLTFVLGLSGFLVWRCRRRSPPPX 114  
Db 61 SDFCLGCAAAPAPAPFLLWPILGGALSLTFVLGLSGFLVWRCRRRREKFTTPI 114  
RESULT 11  
ADD89033  
ID ADD89033 standard; protein; 129 AA.  
XX AC ADD89033;  
XX DT 29-JAN-2004 (first entry)  
XX DE TAT274.  
XX KW tumour-associated antigenic target polypeptide; Cytostatic; tumour;  
XX KW cancer.



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XX OS Homo sapiens.
XX PN WO2003057160-A2.
XX PD 17-JUL-2003.
XX PF 30-DEC-2002; 2002WO-US041798.
XX PR 02-JAN-2002; 2002US-0345444P.
XX PR 25-JAN-2002; 2002US-0351885P.
XX PR 25-FEB-2002; 2002US-0360068P.
XX PR 05-MAR-2002; 2002US-0362004P.
XX PR 20-MAR-2002; 2002US-0366869P.
XX PR 21-MAR-2002; 2002US-0366284P.
XX PR 28-MAR-2002; 2002US-0368679P.
XX PR 19-AUG-2002; 2002US-0404809P.
XX PR 21-AUG-2002; 2002US-0405643P.
XX PA (GETH ) GENENTECH INC.
XX PS Frantz G, Hillan KJ, Phillips H, Polakis P, Smith V, Spencer SD;
XX PI Williams PM, Wu TD, Zhang Z;
XX WPI; 2003-569537/53.
XX DR N-PSDB; ADD89109.
XX PT New antibodies against tumor-associated antigenic target polypeptide,
XX PT useful for treating or diagnosing tumors or cancers in mammals, e.g.
XX PT prostate cancer, lung cancer, prostate adenocarcinomas or renal cell
XX PT carcinomas.
XX PS Claim 1; SEQ ID NO 37; 252pp; English.
XX CC The present invention relates to antibodies against tumour-associated
XX CC antigenic target polypeptide. The antibody is useful for treating or
XX CC diagnosing tumours or cancers in mammals, e.g. prostate cancer, lung
XX CC cancer, breast cancer, colon cancer, ovarian cancer, prostate
XX CC adenocarcinomas, renal cell carcinomas, or pleural mesothelioma. The
XX CC present sequence represents a TAT polypeptide.
XX SQ Sequence 129 AA;

Query Match 94.1%; Score 572; DB 7; Length 129;
Best Local Similarity 93.9%; Pred. No. 1.6e-51;
Matches 107; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 MARGSLRLRLLLVLGLWLLRLSVAGQAPGTAPCSRGSWSADLDKCMDCASCRRAPH 60
DB 1 MARGSLRLRLLLVLGLWLLRLSVAGQAPGTAPCSRGSWSADLDKCMDCASCRRAPH 60
QY 61 SDFCLGCAAAAPPAPRLLPILGGALSLTFVLGLLGLVWRRRCRRSSPPX 114
DB 61 SDFCLGCAAAAPPAPRLLPILGGALSLTFVLGLLGLVWRRRCRRREKFTTPI 114

RESULT 12
ABU64232
ID ABU64232 standard; protein; 129 AA.
XX AC ABU64232;
XX DT 11-MAR-2004 (first entry)
XX DE Human FRADJ protein.
XX KW Metabolic disorder; TNF receptor family member; FRADJ; CRYPTIC; agonist;
XX KW antagonist; gene therapy; vaccine; anorectic; cytostatic; anti-HIV;
XX KW antinflammatory; cardiant; ophthalmological; neuroprotective;
XX KW nephrotropic; antidiabetic; antiarteriosclerotic; hypotensive;
XX KW antilipemic; weight loss; obesity; diabetes.
XX OS Homo sapiens.

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XX WO2003077939-A1.
XX PD 25-SEP-2003.
XX PF 17-MAR-2003; 2003WO-EP050066.
XX PR 19-MAR-2002; 2002US-0365851P.
XX PR 14-MAY-2002; 2002US-0380565P.
XX PA (GBST ) GENSET SA.
XX PI Dialynas D, Lucas J, Scalia A;
XX WPI; 2003-779086/73.
XX DR N-PSDB; AAL56186.
XX PT Use of FRADJ or CRYPTIC polypeptide for preparing a medicament for
XX PT treating or preventing a disorder associated with excessive weight loss
XX PT or an obesity-related disorder.
XX PS Claim 1; Page 200; 206pp; English.
XX CC The present invention provides the human FRADJ and CRYPTIC proteins.
XX CC These can be used in screening for antagonists or agonists of APM1
XX CC polypeptide or polypeptide fragment activity, comprising lipid
XX CC partitioning, lipid metabolism or insulin-like activity. The agonist or
XX CC antagonist of FRADJ or CRYPTIC is useful for preparing a medicament for
XX CC treating or preventing a disorder associated with excessive weight loss,
XX CC comprising cachexia, cancer-related weight loss, AIDS-related weight
XX CC loss, chronic inflammatory disease-related weight loss, bulimia or
XX CC anorexia, or an obesity-related disorder, comprising obesity, insulin
XX CC resistance, atherosclerosis, atheromatous disease, heart disease,
XX CC hypertension, stroke, syndrome x, insulin or non-insulin dependent
XX CC diabetes mellitus, hyperlipidaemia, hyperuricaemia or diabetes-related
XX CC complications, e.g., microangiopathic lesions, ocular lesions, a
XX CC retinopathy, neuropathy or renal lesions. The present sequence is a
XX CC polypeptide shown in the exemplification of the invention
XX SQ Sequence 129 AA;

Query Match 94.1%; Score 572; DB 7; Length 129;
Best Local Similarity 93.9%; Pred. No. 1.6e-51;
Matches 107; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 MARGSLRLRLLLVLGLWLLRLSVAGQAPGTAPCSRGSWSADLDKCMDCASCRRAPH 60
DB 1 MARGSLRLRLLLVLGLWLLRLSVAGQAPGTAPCSRGSWSADLDKCMDCASCRRAPH 60
QY 61 SDFCLGCAAAAPPAPRLLPILGGALSLTFVLGLLGLVWRRRCRRSSPPX 114
DB 61 SDFCLGCAAAAPPAPRLLPILGGALSLTFVLGLLGLVWRRRCRRREKFTTPI 114

RESULT 13
ADN39126
ID ADN39126 standard; protein; 129 AA.
XX AC ADN39126;
XX DT 17-JUN-2004 (first entry)
XX DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:444.
XX KW Human; differential expression; cancer; angiogenic disorder;
XX KW fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
XX KW inflammatory disease; autoimmune disease;
XX KW retinal neovascularisation syndrome; scarring; uterine fibroid;
XX KW detection; diagnosis; prognosis; drug screening; drug targeting;
XX KW wound healing; contraception; cytostatic; cardiant; immunomodulatory;
XX KW vulnerrary; gene therapy; vaccine.
XX OS Homo sapiens.

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XX WO2003042661-A2.
XX PD 22-MAY-2003.
XX PF 13-NOV-2002; 2002WO-US036810.
XX PF 13-NOV-2001; 2001US-0350666P.
XX PR 21-NOV-2001; 2001US-0332464P.
XX PR 09-NOV-2001; 2001US-0334393P.
XX PR 03-DEC-2001; 2001US-0335394P.
XX PR 14-DEC-2001; 2001US-0340376P.
XX PR 08-JAN-2002; 2002US-0347211P.
XX PR 10-JAN-2002; 2002US-0347349P.
XX PR 08-FEB-2002; 2002US-035250P.
XX PR 13-FEB-2002; 2002US-0356714P.
XX PR 20-FEB-2002; 2002US-0359077P.
XX PR 29-MAR-2002; 2002US-0368809P.
XX PR 04-APR-2002; 2002US-0370110P.
XX PR 05-JUN-2002; 2002US-0386614P.
XX PR 16-JUL-2002; 2002US-0396839P.
XX PR 22-JUL-2002; 2002US-039775P.
XX PR 22-JUL-2002; 2002US-0397845P.
XX PR 09-SEP-2002; 2002US-0409450P.
XX PF (EOSB-) EOS BIOTECHNOLOGY INC.
XX PA Afar D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Hevezi PA;
XX PI Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;
XX PF WPI; 2003-468649/44.
XX DR N-PSDB; ADN39125.
XX PT Determining the presence or absence of a pathological cell in a patient,
XX PT useful for diagnosing, prognosing or treating cancer, comprises detecting
XX PT a nucleic acid in a biological sample.
XX PS Claim 12; SEQ ID NO 444; 1385pp; English.
XX CC The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
XX CC whose expression is upregulated or downregulated in specific cancers or
XX CC other diseases such as angiogenic or fibrotic disorders, and to methods
XX CC of determining the presence or absence of a pathological cell in a
XX CC patient by detecting a nucleic acid at least 80% identical to those of
XX CC the invention or by detecting a polypeptide of the invention. The
XX CC invention also relates to expression vectors and host cells comprising a
XX CC nucleic acid of the invention; antibodies which specifically bind a
XX CC polypeptide of the invention; use of such antibodies for drug targeting;
XX CC and methods of screening for modulators of activity or expression of the
XX CC polypeptides and nucleic acids. The nucleic acids, polypeptides,
XX CC antibodies and methods are useful for diagnosing, prognosing and treating
XX CC cancer and other conditions such as psoriasis, ischaemia, heart disease,
XX CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
XX CC Query Match 94.1%; Score 572; DB 7; Length 129;
XX CC Best Local Similarity 93.9%; Pred. No. 1.6e-51;
XX CC Matches 107; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
Qy 1 MARGSLRLLRLVGLWALLRSVAGEQAPGTAPCSRGSSWSADLCKMDCASCRARPH 60
Db 1 MARGSLRLLRLVGLWALLRSVAGEQAPGTAPCSRGSSWSADLCKMDCASCRARPH 60
Qy 61 SDFCLGCAAPAPFRLLWPLILGALSITFVLGSLGFLVWRRCRRERSPPPX 114
Db 61 SDFCLGCAAPAPFRLLWPLILGALSITFVLGSLGFLVWRRCRRERKFTTPI 114
```

## RESULT 14

ADN39987

ID ADN39987 standard; protein; 129 AA.

XX AC

XX AC ADN39987;

XX DT

XX DT 17-JUN-2004 (first entry)

XX DE

XX DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C357.

XX KW

XX KW Human; differential expression; cancer; angiogenic disorder;

XX KW fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;

XX KW inflammatory disease; autoimmune disease;

XX KW retinal neovascularisation syndrome; scarring; uterine fibroid;

XX KW detection; diagnosis; prognosis; drug screening; drug targeting;

XX KW wound healing; contraception; cytostatic; cardiant; immunomodulatory;

XX KW vulnery; gene therapy; vaccine.

XX OS

XX OS Homo sapiens.

XX PN

XX PN WO2003042661-A2.

XX PD

XX PD 22-MAY-2003.

XX PF

XX PF 13-NOV-2002; 2002WO-US036810.

XX PR

XX PR 13-NOV-2001; 2001US-0350666P.

XX PR

XX PR 21-NOV-2001; 2001US-0332464P.

XX PR

XX PR 09-NOV-2001; 2001US-0334393P.

XX PR

XX PR 03-DEC-2001; 2001US-0335394P.

XX PR

XX PR 14-DEC-2001; 2001US-0340376P.

XX PR

XX PR 08-JAN-2002; 2002US-0347211P.

XX PR

XX PR 10-JAN-2002; 2002US-0347349P.

XX PR

XX PR 08-FEB-2002; 2002US-035250P.

XX PR

XX PR 13-FEB-2002; 2002US-0356714P.

XX PR

XX PR 20-FEB-2002; 2002US-0359077P.

XX PR

XX PR 29-MAR-2002; 2002US-0368809P.

XX PR

XX PR 04-APR-2002; 2002US-0370110P.

XX PR

XX PR 05-JUN-2002; 2002US-0386614P.

XX PR

XX PR 16-JUL-2002; 2002US-0396839P.

XX PR

XX PR 22-JUL-2002; 2002US-039775P.

XX PR

XX PR 22-JUL-2002; 2002US-0397845P.

XX PR

XX PR 09-SEP-2002; 2002US-0409450P.

XX PA

XX PA (EOSB-) EOS BIOTECHNOLOGY INC.

XX PI

XX PI Afar D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Hevezi PA;

XX PF

XX PF Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;

XX DR

XX DR WPI; 2003-468649/44.

XX DR

XX DR N-PSDB; ADN39770.

XX PT

XX PT Determining the presence or absence of a pathological cell in a patient,

XX PT useful for diagnosing, prognosing or treating cancer, comprises detecting

XX PT a nucleic acid in a biological sample.

XX PS

XX PS Claim 12; SEQ ID NO C357; 1385pp; English.

XX CC

XX CC The invention relates to nucleic acids and proteins (ADN38683-ADN40064)

XX CC whose expression is upregulated or downregulated in specific cancers or

XX CC other diseases such as angiogenic or fibrotic disorders, and to methods

XX CC of determining the presence or absence of a pathological cell in a

XX CC patient by detecting a nucleic acid at least 80% identical to those of

XX CC the invention or by detecting a polypeptide of the invention. The

XX CC invention also relates to expression vectors and host cells comprising a

XX CC nucleic acid of the invention; antibodies which specifically bind a

XX CC polypeptide of the invention; use of such antibodies for drug targeting;

XX CC and methods of screening for modulators of activity or expression of the

XX CC polypeptides and nucleic acids. The nucleic acids, polypeptides,

XX CC antibodies and methods are useful for diagnosing, prognosing and treating

XX CC cancer and other conditions such as psoriasis, ischaemia, heart disease,

XX CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal

CC neovascularisation syndromes, scarring and uterine fibroids. They may  
CC also be useful in wound healing and in contraception. The present  
CC sequence represents a polypeptide of the invention.

XX  
SQ Sequence 129 AA;

Query Match 94.1%; Score 572; DB 7; Length 129;

Best Local Similarity 93.9%; Pred. NO. 1.6e-51;

Matches 107; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 MARGSLRLLRLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRRAPH 60

Db 1 MARGSLRLLRLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRRAPH 60

QY 61 SDFCLGCAAAAPPAPFRLLPILGGALSLTFVLGLLSGFLVWRCRRERSPPPX 114

Db 61 SDFCLGCAAAAPPAPFRLLPILGGALSLTFVLGLLSGFLVWRCRRERSPPPX 114

RESULT 15

ABM81706

ID ABM81706 standard; protein; 129 AA.

XX

AC ABM81706;

XX

DT 18-NOV-2004 (first entry)

XX

DE Tumour-associated antigenic target (TAT) polypeptide PRO12683, SEQ:4399.

XX

KW Tumour-associated antigenic target; TAT; human; overexpression; cancer;

KW tumour; diagnosis; cell proliferative disorder; breast cancer;

KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;

KW central nervous system cancer; bladder cancer; pancreatic cancer;

KW cervical cancer; melanoma; leukaemia; hybridisation probe;

KW chromosome identification; chromosome mapping; gene mapping;

KW gene therapy; cytostatic.

XX

OS Homo sapiens.

XX

PN WO2004030615-A2.

XX

PD 15-APR-2004.

XX

PF 29-SEP-2003; 2003WO-US028547.

XX

PR 02-OCT-2002; 2002US-0414971P.

XX

PA (GETH ) GENENTECH INC.

XX

PI Wu TD, Zhang Z, Zhou Y;

XX

DR WPI; 2004-347921/32.

XX

DR N-PSDB; ACN39936.

XX

PT New tumor-associated antigenic target polypeptides and nucleic acids,

PT useful in preparing a medicament for treating or detecting a

PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or

PT prostate cancer or tumor.

XX

PS Claim 12; SEQ ID NO 4399; 7273pp; English.

XX

CC The invention relates to human tumour-associated antigenic target (TAT)

CC polypeptides, and their related nucleic acids. The TAT polypeptides are

CC overexpressed in cancer tissues compared to normal tissues, and may thus

CC serve as effective targets for the diagnosis and treatment of cancer in

CC mammals. The invention also relates to nucleic acid and polypeptide

CC sequences at least 80% identical to the TAT nucleic acids and

CC polypeptides; expression vectors and host cells comprising a TAT nucleic

CC acid; an antibody specific for a TAT polypeptide; a peptide or organic

CC molecule which binds to a TAT polypeptide; fusion proteins comprising a

CC TAT polypeptide; and methods and compositions for the treatment or

CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,

CC antibodies, antagonists, binding molecules and compositions are useful

CC for diagnosing or treating a cell proliferative disorder associated with  
CC increased TAT expression, particularly cancers such as breast cancer,  
CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder  
CC cancer, pancreatic cancer, cervical cancer, cancers of the central  
CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be  
CC used as hybridisation probes, in chromosome and gene mapping, in  
CC chromosome identification and in gene therapy. The present sequence  
CC represents a TAT polypeptide of the invention

XX Sequence 129 AA;

Query Match 94.1%; Score 572; DB 8; Length 129;

Best Local Similarity 93.9%; Pred. NO. 1.6e-51;

Matches 107; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 MARGSLRLLRLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRRAPH 60

Db 1 MARGSLRLLRLVLGLWLALLRSVAGEQAPGTAPCSRGSSWSADLDKCMDCASCRRAPH 60

QY 61 SDFCLGCAAAAPPAPFRLLPILGGALSLTFVLGLLSGFLVWRCRRERSPPPX 114

Db 61 SDFCLGCAAAAPPAPFRLLPILGGALSLTFVLGLLSGFLVWRCRRERSPPPX 114

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Job time : 167 secs

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GenCore version 5.1.6  
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# OM protein - protein search, using sw model

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(without alignments)  
288.755 Million cell updates/sec

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Perfect score: 608  
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Gapop 10.0 , Gapext 0.5

Searched: 1376875 seqs, 326749119 residues

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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4	572	94.1	129	9	US-09-883-777-4
5	572	94.1	129	14	US-10-044-298A-178
6	572	94.1	129	14	US-10-042-211A-178
7	572	94.1	129	15	US-10-331-496A-37
8	572	94.1	129	15	US-10-295-027-444
9	572	94.1	129	15	US-10-295-027-1305
10	572	94.1	129	15	US-10-617-217A-178
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12	451	74.2	129	9	US-09-883-777-5
13	433	71.2	309	9	US-09-742-454A-7

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15	379.5	62.4	300	9	US-09-883-777-9
16	274.5	45.1	112	15	US-10-351-334-139
17	274.5	45.1	155	15	US-10-351-334-284
18	274.5	45.1	156	15	US-10-351-334-228
19	97.5	16.0	171	14	US-10-251-947-4
20	97.5	16.0	171	14	US-10-251-947-7
21	97.5	16.0	185	14	US-10-251-947-2
22	97	16.0	170	14	US-10-251-947-6
23	89.5	14.7	185	15	US-10-380-703-5
24	89.5	14.7	1307	14	US-10-303-685-17
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31	88	14.5	266	15	US-10-380-703-7
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33	87.5	14.4	186	14	US-10-251-947-14
34	87	14.3	426	15	US-10-257-174-44
35	87	14.3	426	15	US-10-343-357-6
36	85	14.0	872	16	US-10-437-963-111595
37	84	13.8	152	16	US-10-767-701-33810
38	81	13.3	484	16	US-10-437-963-162231
39	79.5	13.1	377	14	US-10-156-761-8962
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## ALIGNMENTS

### RESULT 1

US-10-062-831-59  
; Sequence 59, Application US/10062831  
; Publication No. US20030105297A1  
; GENERAL INFORMATION:  
; APPLICANT: Steven M. Ruben, et al.  
; TITLE OF INVENTION: 32 Human Secreted Proteins  
; FILE REFERENCE: P2006P1  
; CURRENT APPLICATION NUMBER: US/10/062,831  
; PRIOR FILING DATE: 2002-02-05  
; PRIOR APPLICATION NUMBER: 09/690,454  
; PRIOR FILING DATE: 1998-11-10  
; PRIOR APPLICATION NUMBER: PCT/US98/10868  
; PRIOR FILING DATE: May 28, 1998  
; PRIOR APPLICATION NUMBER: 60/044,039  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/048,093  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/048,190  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/050,935  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/048,101  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/048,356  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/056,250  
; PRIOR FILING DATE: August 29, 1997  
; PRIOR APPLICATION NUMBER: 60/056,296  
; PRIOR FILING DATE: August 29, 1997  
; PRIOR APPLICATION NUMBER: 60/056,293  
; PRIOR FILING DATE: August 29, 1997  
; NUMBER OF SEQ ID NOS: 229  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 59  
; LENGTH: 114

Sequence 7, Appli  
Sequence 9, Appli  
Sequence 139, App  
Sequence 284, App  
Sequence 228, App  
Sequence 4, Appli  
Sequence 7, Appli  
Sequence 2, Appli  
Sequence 6, Appli  
Sequence 5, Appli  
Sequence 17, Appli  
Sequence 138, App  
Sequence 140, App  
Sequence 984, App  
Sequence 2, Appli  
Sequence 60, Appli  
Sequence 10, Appli  
Sequence 7, Appli  
Sequence 154909,  
Sequence 14, Appli  
Sequence 44, Appli  
Sequence 6, Appli  
Sequence 111595,  
Sequence 33810, A  
Sequence 162231,  
Sequence 8962, Ap  
Sequence 181815,  
Sequence 31, Appli  
Sequence 31, Appli  
Sequence 26, Appli  
Sequence 26, Appli  
Sequence 5, Appli

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; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (114)
; OTHER INFORMATION: Xaa equals stop translation
US-10-062-831-59

Query Match      100.0%; Score 608; DB 14; Length 114;
Best Local Similarity 100.0%; Pred. No. 4.6e-50;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MARGSLRLRLLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRPH 60
Db      1 MARGSLRLRLLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRPH 60

Qy      61 SDFCLGCAAAAPPAPFLLWPILGALSITFVLGSLGFLVWRCRRRSSPPPX 114
Db      61 SDFCLGCAAAAPPAPFLLWPILGALSITFVLGSLGFLVWRCRRRSSPPPX 114

RESULT 2
US-10-062-599-59
; Sequence 59, Application US/10062599
; Publication No. US20030195346A1
; GENERAL INFORMATION:
; APPLICANT: Steven M. Ruben, et al.
; TITLE OF INVENTION: 32 Human Secreted Proteins
; FILE REFERENCE: P2006P1
; CURRENT APPLICATION NUMBER: US/10/062,599
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: 09/690,454
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: 09/189,144
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 60/044,039
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,093
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,101
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,356
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/056,250
; PRIOR FILING DATE: August 29, 1997
; PRIOR APPLICATION NUMBER: 60/056,296
; PRIOR FILING DATE: August 29, 1997
; PRIOR APPLICATION NUMBER: 60/056,293
; PRIOR FILING DATE: August 29, 1997
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 59
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (114)
; OTHER INFORMATION: Xaa equals stop translation
US-10-062-599-59

Query Match      100.0%; Score 608; DB 14; Length 114;
Best Local Similarity 100.0%; Pred. No. 4.6e-50;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 MARGSLRLRLLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRPH 60
Db      1 MARGSLRLRLLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRPH 60
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Qy      61 SDFCLGCAAAAPPAPFLLWPILGALSITFVLGSLGFLVWRCRRRSSPPPX 114
Db      61 SDFCLGCAAAAPPAPFLLWPILGALSITFVLGSLGFLVWRCRRRSSPPPX 114

RESULT 3
US-09-742-454A-4
; Sequence 4, Application US/09742454A
; Patent No. US20020041876A1
; GENERAL INFORMATION:
; APPLICANT: WILEY, Steven R.
; TITLE OF INVENTION: TWEAK Receptor
; FILE REFERENCE: 2968-B
; CURRENT APPLICATION NUMBER: US/09/742,454A
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: 60/203,347
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-742-454A-4

Query Match      94.1%; Score 572; DB 9; Length 129;
Best Local Similarity 93.9%; Pred. No. 1.3e-46;
Matches 107; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy      1 MARGSLRLRLLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRPH 60
Db      1 MARGSLRLRLLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRPH 60

Qy      61 SDFCLGCAAAAPPAPFLLWPILGALSITFVLGSLGFLVWRCRRRSSPPPX 114
Db      61 SDFCLGCAAAAPPAPFLLWPILGALSITFVLGSLGFLVWRCRRREKFTTPI 114

RESULT 4
US-09-883-777-4
; Sequence 4, Application US/09883777
; Patent No. US20020110853A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: TWEAK RECEPTOR
; FILE REFERENCE: 2968-C
; CURRENT APPLICATION NUMBER: US/09/883,777
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: US 60/203,347
; PRIOR FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: PCT/US00/34755
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/742,454
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 129
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-883-777-4

Query Match      94.1%; Score 572; DB 9; Length 129;
Best Local Similarity 93.9%; Pred. No. 1.3e-46;
Matches 107; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy      1 MARGSLRLRLLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRPH 60
Db      1 MARGSLRLRLLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRPH 60
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QY	61	SDFCLGCAAPAPPFLLWPIIGGALSITFVLGLISGLVWRCRRSSPPX	114
Db	61	SDFCLGCAAPAPPFLLWPIIGGALSITFVLGLISGLVWRCRRKEFTPI	114

## RESULT 5

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US-10-024-298A-178
; Sequence 178, Application US/10024298A
; Publication No. US20030143540A1
; GENERAL INFORMATION:
; APPLICANT: ASAHI KASEI KABUSHIKI KAISHA
; APPLICANT: AKIO MATSUDA
; APPLICANT: Goichi HONDA
; APPLICANT: Shuji MURAMATSU
; APPLICANT: Yukiko NAGANO
; TITLE OF INVENTION: NF-K B Activating Gene
; FILE REFERENCE: 1254-0191P
; CURRENT APPLICATION NUMBER: US/10/024,298A
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/314,385
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/278,641
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/258,315
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP254018/2001
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: JP0088912/2001
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: JP402288/2000
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 162
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 178
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-024-298A-178

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	Query Match	94.1%	Score 572;	DB 14;	Length 129;
	Best Local Similarity	93.9%	Pred. No. 1.3e-46;		
	Matches 107;	Conservative 1;	Mismatches 6;	Indels 0;	Gaps 0;
Qy	1	MARGSLRRLLRLVLGLWLLALLRSVAGEQAPGTAPCSRGSSWSADLQKCMDCASCARPH	60		
Db	1	MARGSLRRLLRLVLGLWLLALLRSVAGEQAPGTAPCSRGSSWSADLQKCMDCASCARPH	60		
Qy	61	SDFCLGCAAAAPPAPFRLIWLPIILGALSILTFVLGLLSGLVWRRCRRRSSPPX	114		
Db	61	SDFCLGCAAAAPPAPFRLIWLPIILGALSILTFVLGLLSGLVWRRCRRRKFTPTI	114		

RESIST. 6

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RES-201-0
US-201-042-211A-178
; Sequence 178, Application US/10042211A
; Publication No. US20030170719A1
;
; GENERAL INFORMATION:
;
; APPLICANT: MATSUDA, Akio et al.
;
; TITLE OF INVENTION: NFkB Activating Gene
;
; FILING DATE: 1254-0132P
;
; CURRENT APPLICATION NUMBER: US/10/042,211A
;
; CURRENT FILING DATE: 2002-01-11
;
; PRIOR APPLICATION NUMBER: JP 2000-402288
;
; PRIOR FILING DATE: 2000-12-28
;
; PRIOR APPLICATION NUMBER: JP 2001-088912
;
; PRIOR FILING DATE: 2001-03-26
;
; PRIOR APPLICATION NUMBER: JP 2001-254018
;
; PRIOR FILING DATE: 2001-08-24
;
; PRIOR APPLICATION NUMBER: US 60/258,315
;
; PRIOR FILING DATE: 2000-12-28
;
; PRIOR APPLICATION NUMBER: US 60/278,640
;
; PRIOR FILING DATE: 2001-03-26

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; PRIOR APPLICATION NUMBER: US 60/314,385
; PRIOR FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 178
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-042-211A-178

Query Match          94.1%;   Score 572;   DB 14;   Length 129;
Best Local Similarity 93.9%;   Pred. No. 1.3e-46;
Matches 107;   Conservative 1;   Mismatches 6;   Indels 0;   Gaps 0;

Qy      1  MARGSRRLRLRLVLGLWLLALLSVAGEAGPTAPCSRGSWSGADLLDKWDCASCRRAPH 60
        |||||||
Db      1  MARGSRRLRLRLVLGLWLLALLSVAGEAGPTAPCSRGSWSGADLLDKWDCASCRRAPH 60

Qy      61  SDFCLGCAAAPAFRLLPILGALSLTFVLGLLSGFLVRRRCRRRSPPPX 114
        |||||||
Db      61  SDFCLGCAAAPAFRLLPILGALSLTFVLGLLSGFLVRRRCRRREKETPI 114
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## RESULTS

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US-10-331-496A-37
; Sequence 37, Application US/10331496A
; Publication No. US20030228305A1
; GENERAL INFORMATION:
; APPLICANT: FRANTZ,GRETCHEN
; APPLICANT: HILLAN,KENNETH J.
; APPLICANT: PHILLIPS,HEIDI S.
; APPLICANT: FOLAKIS,PAUL
; APPLICANT: SMITH,VICTORIA
; APPLICANT: SPENCER,SUSAN D.
; APPLICANT: WILLIAMS,P. MICKEY
; APPLICANT: WU,THOMAS D.
; APPLICANT: ZHANG,ZEMIN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF TUMOR
; FILE REFERENCE: P501491-PCT
; CURRENT APPLICATION NUMBER: US/10/331.496A
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 60/345,444
; PRIOR FILING DATE: 2002-01-02
; PRIOR APPLICATION NUMBER: US 60/351,885
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: US 60/360,066
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: US 60/362,004
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/366,869
; PRIOR FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: US 60/366,284
; PRIOR FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: US 60/368,679
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 60/404,809
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/405,645
; PRIOR FILING DATE: 2002-08-21
; NUMBER OF SEQ ID NOS: 95
; SEQ ID NO 37
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapien
; US-10-331-496A-37

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Query Match      94.1%; Score 572; DB 15; Length 129;
Best Local Similarity 93.9%; Pred. No. 1.3e-46;
Matches 107; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy      1  MARGSRLLRLRLVLGLWLLALLSVAGEQAPGTAPCRGSGWSADLDKCMWDCASCRARPH 60

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Db 1 MARGSLRLLRLVLGLWLLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCARPH 60
Qy 61 SDFCLGCAAAAPPAPFRLLPILGALSLTFVLGLSGFLVWRCRRRSSPPPX 114
Db 61 SDFCLGCAAAAPPAPFRLLPILGALSLTFVLGLSGFLVWRCRRRREKFTTPI 114

RESULT 8
US-10-295-027-444
; Sequence 444, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Gineberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-13
; PRIOR APPLICATION NUMBER: US 60/356,714
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 444
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-444

Query Match 94.1%; Score 572; DB 15; Length 129;
Best Local Similarity 93.9%; Pred. No. 1.3e-46;
Matches 107; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MARGSLRLLRLVLGLWLLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCARPH 60
Db 1 MARGSLRLLRLVLGLWLLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCARPH 60

Qy 61 SDFCLGCAAAAPPAPFRLLPILGALSLTFVLGLSGFLVWRCRRRSSPPPX 114
Db 61 SDFCLGCAAAAPPAPFRLLPILGALSLTFVLGLSGFLVWRCRRRREKFTTPI 114

RESULT 9
US-10-295-027-1305
; Sequence 1305, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Gineberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-13
; PRIOR APPLICATION NUMBER: US 60/356,714
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 444
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-444

Query Match 94.1%; Score 572; DB 15; Length 129;
Best Local Similarity 93.9%; Pred. No. 1.3e-46;
Matches 107; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MARGSLRLLRLVLGLWLLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCARPH 60
Db 1 MARGSLRLLRLVLGLWLLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCARPH 60

Qy 61 SDFCLGCAAAAPPAPFRLLPILGALSLTFVLGLSGFLVWRCRRRSSPPPX 114
Db 61 SDFCLGCAAAAPPAPFRLLPILGALSLTFVLGLSGFLVWRCRRRREKFTTPI 114
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; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Gineberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-13
; PRIOR APPLICATION NUMBER: US 60/356,714
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1305
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-1305

Query Match 94.1%; Score 572; DB 15; Length 129;
Best Local Similarity 93.9%; Pred. No. 1.3e-46;
Matches 107; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MARGSLRLLRLVLGLWLLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCARPH 60
Db 1 MARGSLRLLRLVLGLWLLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCARPH 60

Qy 61 SDFCLGCAAAAPPAPFRLLPILGALSLTFVLGLSGFLVWRCRRRSSPPPX 114
Db 61 SDFCLGCAAAAPPAPFRLLPILGALSLTFVLGLSGFLVWRCRRRREKFTTPI 114

RESULT 10
US-10-617-217A-178
; Sequence 178, Application US/10617217A
; Publication No. US20040081986A1
; GENERAL INFORMATION:
; APPLICANT: MATSUDA, Akio et al.
; TITLE OF INVENTION: NP-KB ACTIVATING GENE
; FILE REFERENCE: 1254-0229P
; CURRENT APPLICATION NUMBER: US/10/617,217A
; CURRENT FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: JP 2000-402288
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP 2001-088912
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: JP 2001-254018
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;; PRIOR FILING DATE: 2001-08-24  
;; PRIOR APPLICATION NUMBER: US 60/258,315  
;; PRIOR FILING DATE: 2000-12-28  
;; PRIOR APPLICATION NUMBER: US 60/278,640  
;; PRIOR FILING DATE: 2001-03-26  
;; PRIOR APPLICATION NUMBER: US 60/314,385  
;; PRIOR FILING DATE: 2001-08-24  
;; PRIOR APPLICATION NUMBER: US 09/883,777  
;; NUMBER OF SEQ ID NOS: 224  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 178  
;; LENGTH: 129  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-617-217A-178

Query Match 94.1%; Score 572; DB 15; Length 129;  
Best Local Similarity 93.9%; Pred. No. 1.3e-46;  
Matches 107; Conservative 1; Mismatches 6; Indels 0; Gaps 0;  
QY 1 MARGSLRLLRLVLLGLWLLALLRSVAGEQAPCTAPCSRGSWSADLDKCMDCASCARPH 60  
Db 1 MARGSLRLLRLVLLGLWLLALLRSVAGEQAPCTAPCSRGSWSADLDKCMDCASCARPH 60  
QY 61 SDFCLGCAAAPAPPAPFRLWLPILGGALSLTFVLGSLGFLVWRCRRRSPPPX 114  
Db 61 SDFCLGCAAAPAPPAPFRLWLPILGGALSLTFVLGSLGFLVWRCRRRREKFTTPI 114

RESULT 11  
US-09-742-454A-5  
;; Sequence 5, Application US/09742454A  
;; Patent No. US20020041876A1  
;; GENERAL INFORMATION:  
;; APPLICANT: WILEY, Steven R.  
;; TITLE OF INVENTION: TWEAK Receptor  
;; FILE REFERENCE: 2968-B  
;; CURRENT APPLICATION NUMBER: US/09/742,454A  
;; CURRENT FILING DATE: 2000-12-19  
;; PRIOR APPLICATION NUMBER: 60/172,878  
;; PRIOR FILING DATE: 1999-12-20  
;; PRIOR APPLICATION NUMBER: 60/203,347  
;; PRIOR FILING DATE: 2000-05-10  
;; NUMBER OF SEQ ID NOS: 7  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 5  
;; LENGTH: 129  
;; TYPE: PRT  
;; ORGANISM: Mus sp.  
US-09-742-454A-5

Query Match 74.2%; Score 451; DB 9; Length 129;  
Best Local Similarity 74.6%; Pred. No. 4e-35;  
Matches 85; Conservative 7; Mismatches 22; Indels 0; Gaps 0;  
QY 1 MARGSLRLLRLVLLGLWLLALLRSVAGEQAPCTAPCSRGSWSADLDKCMDCASCARPH 60  
Db 1 MAPGWRSLPQILVLGFLVLMRAAAGEQAPCTSPCSSGSSWSADLDKCMDCASCARPH 60  
QY 61 SDFCLGCAAAPAPPAPFRLWLPILGGALSLTFVLGSLGFLVWRCRRRSPPPX 114  
Db 61 SDFCLGCAAAPAPPAPFRLWLPILGGALSLTFVLGSLGFLVWRCRRRREKFTTPI 114

RESULT 12  
US-09-883-777-5  
;; Sequence 5, Application US/09883777  
;; Patent No. US20020110853A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Wiley, Steven R.  
;; TITLE OF INVENTION: TWEAK RECEPTOR  
;; FILE REFERENCE: 2968-C  
;; CURRENT APPLICATION NUMBER: US/09/883,777  
;; CURRENT FILING DATE: 2001-06-18

;; PRIOR APPLICATION NUMBER: US 60/172,878  
;; PRIOR FILING DATE: 1999-12-20  
;; PRIOR APPLICATION NUMBER: US 60/203,347  
;; PRIOR FILING DATE: 2000-05-10  
;; PRIOR APPLICATION NUMBER: PCT/US00/34755  
;; PRIOR FILING DATE: 2000-12-19  
;; PRIOR APPLICATION NUMBER: US 09/742,454  
;; PRIOR FILING DATE: 2000-12-19  
;; NUMBER OF SEQ ID NOS: 16  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 5  
;; LENGTH: 129  
;; TYPE: PRT  
;; ORGANISM: Mus sp.  
US-09-883-777-5

Query Match 74.2%; Score 451; DB 9; Length 129;  
Best Local Similarity 74.6%; Pred. No. 4e-35;  
Matches 85; Conservative 7; Mismatches 22; Indels 0; Gaps 0;  
QY 1 MARGSLRLLRLVLLGLWLLALLRSVAGEQAPCTAPCSRGSWSADLDKCMDCASCARPH 60  
Db 1 MAPGWRSLPQILVLGFLVLMRAAAGEQAPCTSPCSSGSSWSADLDKCMDCASCARPH 60  
QY 61 SDFCLGCAAAPAPPAPFRLWLPILGGALSLTFVLGSLGFLVWRCRRRSPPPX 114  
Db 61 SDFCLGCAAAPAPPAPFRLWLPILGGALSLTFVLGSLGFLVWRCRRRREKFTTPI 114

RESULT 13  
US-09-742-454A-7  
;; Sequence 7, Application US/09742454A  
;; Patent No. US20020041876A1  
;; GENERAL INFORMATION:  
;; APPLICANT: WILEY, Steven R.  
;; TITLE OF INVENTION: TWEAK Receptor  
;; FILE REFERENCE: 2968-B  
;; CURRENT APPLICATION NUMBER: US/09/742,454A  
;; CURRENT FILING DATE: 2000-12-19  
;; PRIOR APPLICATION NUMBER: 60/172,878  
;; PRIOR FILING DATE: 1999-12-20  
;; PRIOR APPLICATION NUMBER: 60/203,347  
;; PRIOR FILING DATE: 2000-05-10  
;; NUMBER OF SEQ ID NOS: 7  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 7  
;; LENGTH: 309  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence: human TWEAK  
;; OTHER INFORMATION: receptor fusion protein construct  
US-09-742-454A-7

Query Match 71.2%; Score 433; DB 9; Length 309;  
Best Local Similarity 74.1%; Pred. No. 4.7e-33;  
Matches 83; Conservative 2; Mismatches 5; Indels 22; Gaps 1;  
QY 1 MARGSLRLLRLVLLGLWLLALLRSVAGEQAPCTAPCSRGSWSADLDKCMDCASCARPH 60  
Db 1 MARGSLRLLRLVLLGLWLLALLRSVAGEQAPCTAPCSRGSWSADLDKCMDCASCARPH 60  
QY 61 SDFCLGCAAAPAPPAPFRLWLPILGGALSLTFVLGSLGFLVWRCRRRSPPPX 112  
Db 61 SDFCLGCAAAPAPPAPFRLWLPILGGALSLTFVLGSLGFLVWRCRRRREKFTTPI 90

RESULT 14  
US-09-883-777-7  
;; Sequence 7, Application US/09883777  
;; Patent No. US20020110853A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Wiley, Steven R.

Db 61 SDFCLGCAAAARSCDKTHTCTCPP 83  
 Search completed: February 14, 2005, 06:59:18  
 Job time : 130 secs

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; TITLE OF INVENTION: TWEAK RECEPTOR
; FILE REFERENCE: 2968-C
; CURRENT APPLICATION NUMBER: US/09/883,777
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: US 60/203,347
; PRIOR FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: PCT/US00/34755
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/742,454
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human TWEAK receptor fusion protein construct
US-09-883-777-7

Query Match 71.2%; Score 433; DB 9; Length 309;
Best Local Similarity 74.1%; Pred. No. 4.7e-33;
Matches 83; Conservative 2; Mismatches 5; Indels 22; Gaps 1;

QY 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRAPH 60
Db 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRAPH 60
QY 61 SDFCLGCAAAAPAPPRLLWPLILGGALSLTFVLGLLSGFLVMRCRRERSPP 112
Db 61 SDFCLGCAAAAPAPPRLL-----WRSCKTHTCTCP 90

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RESULT 15
US-09-883-777-9
; Sequence 9, Application US/09883777
; Patent No. US20020110853A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: TWEAK RECEPTOR
; FILE REFERENCE: 2968-C
; CURRENT APPLICATION NUMBER: US/09/883,777
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: US 60/203,347
; PRIOR FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: PCT/US00/34755
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/742,454
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human TWEAK receptor fusion protein construct
US-09-883-777-9

Query Match 62.4%; Score 379.5; DB 9; Length 300;
Best Local Similarity 88.0%; Pred. No. 5.4e-28;
Matches 73; Conservative 0; Mismatches 1; Indels 9; Gaps 1;

QY 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRAPH 60
Db 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRAPH 60
QY 61 SDFCLGCAAA-----PPAP 74

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 14, 2005, 06:36:43 ; Search time 43 Seconds  
(without alignments)  
197.907 Million cell updates/sec

Title: US-10-062-831-59  
Perfect score: 608  
Sequence: 1 MARGSLRLLVLLGLWLA.....LSGFLVWRCRRSSPPPX 114

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: /cgm2\_6/ptodata/1/iaa/6A\_COMB.pep:\*  
4: /cgm2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
5: /cgm2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
6: /cgm2\_6/ptodata/1/iaa/backfiles.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	572	94.1	129	4	US-09-883-777-4
3	572	94.1	129	4	US-09-949-016-6914
4	572	94.1	129	4	US-09-742-454A-4
5	451	74.2	129	4	US-09-883-777-5
6	451	74.2	129	4	US-09-742-454A-5
7	433	71.2	309	4	US-09-883-777-7
8	433	71.2	309	4	US-09-742-454A-7
9	379.5	62.4	300	4	US-09-883-777-9
10	274.5	45.1	112	4	US-09-489-847-139
11	274.5	45.1	155	4	US-09-489-847-284
12	274.5	45.1	156	4	US-09-489-847-228
13	96.5	15.9	248	4	US-09-252-991A-29249
14	88.5	14.6	400	4	US-09-252-991A-26145
15	87.5	14.4	631	4	US-09-252-991A-20063
16	83.5	13.7	152	4	US-09-252-991A-31619
17	80.5	13.2	249	4	US-09-252-991A-29850
18	77	12.7	250	4	US-09-322-409-31
19	77	12.7	250	4	US-09-451-527-31
20	77	12.7	276	4	US-09-322-409-26
21	77	12.7	276	4	US-09-451-527-26
22	75	12.3	334	4	US-09-252-991A-18795
23	74.5	12.3	305	4	US-09-252-991A-21147
24	73.5	12.1	187	3	US-09-199-637A-287
25	73.5	12.1	187	4	US-09-252-991A-21454
26	72.5	11.9	365	4	US-09-949-016-6907
27	72.5	11.9	391	4	US-09-949-016-7325

ALIGNMENTS

RESULT 1

US-09-690-454-59  
; Sequence 59, Application US/09690454  
; Patent No. 6531447  
; GENERAL INFORMATION:  
; APPLICANT: Steven M. Ruben, et al.  
; TITLE OF INVENTION: 32 Human Secreted Proteins  
; FILE REFERENCE: PZ006P1  
; CURRENT APPLICATION NUMBER: US/09/690,454  
; CURRENT FILING DATE: 2000-10-18  
; PRIOR APPLICATION NUMBER: 09/189,144  
; PRIOR FILING DATE: 1998-11-10  
; PRIOR APPLICATION NUMBER: 60/044,039  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/048,093  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/048,190  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/050,935  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/048,101  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/048,356  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/056,250  
; PRIOR FILING DATE: August 29, 1997  
; PRIOR APPLICATION NUMBER: 60/056,296  
; PRIOR FILING DATE: August 29, 1997  
; PRIOR APPLICATION NUMBER: 60/056,293  
; PRIOR FILING DATE: August 29, 1997  
; NUMBER OF SEQ ID NOS: 229  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 59  
; LENGTH: 114  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (114)  
; OTHER INFORMATION: Xaa equals stop translation  
US-09-690-454-59

Query Match 100.0%; Score 608; DB 4; Length 114;  
Best Local Similarity 100.0%; Pred.No. 6e-58;  
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MARGSLRLLVLLGLWLA...LSGFLVWRCRRSSPPPX 60



RESULT 7  
US-09-883-777-7  
; Sequence 7, Application US/09883777  
; Patent No. 672725  
; GENERAL INFORMATION:  
; APPLICANT: Wiley, Steven R.  
; TITLE OF INVENTION: TWEAK RECEPTOR  
; FILE REFERENCE: 2968-C  
; CURRENT APPLICATION NUMBER: US/09/883,777  
; CURRENT FILING DATE: 2001-06-18  
; PRIOR APPLICATION NUMBER: US 60/172,878  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: US 60/203,347  
; PRIOR FILING DATE: 2000-05-10  
; PRIOR APPLICATION NUMBER: PCT/US00/34755  
; PRIOR FILING DATE: 2000-12-19  
; PRIOR APPLICATION NUMBER: US 09/742,454  
; PRIOR FILING DATE: 2000-12-19  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7  
; LENGTH: 309  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Human TWEAK receptor fusion protein construct  
US-09-883-777-7

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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human TWEAK receptor fusion protein construct
US-09-883-777-9

Query Match          62.4%; Score 379.5; DB 4; Length 300;
Best Local Similarity 88.0%; Pred. No. 6.5e-33;
Matches 73; Conservative 0; Mismatches 1; Indels 9; Gaps 1;

Qy 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCA-SC 60
Db 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCA-SC 60

Qy 61 SDFCLGCAAA-----PPAP 74
Db 61 SDFCLGCAAAARCDKTHTCPCP 83

RESULT 10
US-09-489-847-139
; Sequence 139, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: P2031P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 139
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-489-847-139

Query Match          45.1%; Score 274.5; DB 4; Length 112;
Best Local Similarity 96.4%; Pred. No. 4e-22;
Matches 54; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCA-SC 55
Db 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCTSC 56

RESULT 11
US-09-489-847-284
; Sequence 284, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: P2031P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
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; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 284
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-489-847-284

Query Match          45.1%; Score 274.5; DB 4; Length 155;
Best Local Similarity 96.4%; Pred. No. 5.8e-22;
Matches 54; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCA-SC 55
Db 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCTSC 56

RESULT 12
US-09-489-847-228
; Sequence 228, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: P2031P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 228
; LENGTH: 156
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (156)
; OTHER INFORMATION: Xaa equals stop translation
US-09-489-847-228

Query Match          45.1%; Score 274.5; DB 4; Length 156;
Best Local Similarity 96.4%; Pred. No. 5.8e-22;
Matches 54; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCA-SC 55
Db 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCTSC 56

RESULT 13
US-09-252-991A-29249
; Sequence 29249, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
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RESULT 15
US-09-252-991A-20063
; Sequence 20063, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 14, 2005, 06:57:11 ; Search time 38 Seconds  
(without alignments)  
288.650 Million cell updates/sec

Title: US-10-062-831-59  
Perfect score: 608  
Sequence: 1 MARGSLRLRLVLGLWLA.....LSGFLVWRRCRRSSPPPX 114

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 9621673 residues

Total number of hits satisfying chosen parameters: 47647

Minimum DB seq length: 0  
Maximum DB seq length: 114

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	64	10.5	108	2 T49319	hypothetical prote
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3	61	10.0	55	1 PERE	ferredoxin 2(fdx-4)
4	61	10.0	66	2 S58086	metallothionein 3
5	61	10.0	68	2 I67866	growth inhibitory
6	61	10.0	68	2 A46034	metallothionein 3
7	60.5	10.0	76	2 T03860	TA20 protein - com
8	59	9.7	68	2 B46034	metallothionein 3
9	58.5	9.6	78	2 E69969	hypothetical prote
10	58	9.5	36	2 C45875	M1 class I histoco
11	58	9.5	68	2 S44391	metallothionein 3
12	57.5	9.5	92	2 T04395	probable phospholi
13	57	9.4	101	2 T26641	hypothetical prote
14	57	9.4	107	2 G72496	hypothetical prote
15	56.5	9.3	67	2 G82702	hypothetical prote
16	56.5	9.3	95	2 T06275	benzothiadiazole-1
17	56.5	9.3	109	2 E84202	ferredoxin [import
18	56	9.2	103	2 T08775	hypothetical prote
19	55.5	9.1	58	2 C69365	ferredoxin (fdx-5)
20	55.5	9.1	59	1 FEDV2N	ferredoxin 2(fdx-4)
21	55.5	9.1	85	2 H93303	hypothetical prote
22	55.5	9.1	111	2 A85866	hypothetical prote
23	55	9.0	114	2 A13204	IS66 family orf2 [
24	54	8.9	105	2 C72608	hypothetical prote
25	54	8.9	110	2 A55991	effector cell prot
26	53.5	8.8	38	2 PS0133	H-2 class I histoc
27	53.5	8.8	81	2 S39511	photosystem I iron
28	53.5	8.8	97	2 A51270	ferredoxin [import
29	53	8.7	59	2 IS1272	retinoic acid rece

ALIGNMENTS

RESULT 1

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C:Species: Neurospora crassa  
C:Date: 02-Jun-2000 #sequence\_revision 02-Jun-2000 #text\_change 02-Jun-2000  
C:Accession: T49319  
R:Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, May 2000  
A:Reference number: Z25022  
A:Accession: T49319  
A:Status: preliminary  
A:Accession: T49319  
A:Molecule type: DNA  
A:Residues: 1-108 <SCH>  
A:Cross-references: EMBL:AL355925; GSPDB:GN00116; NCSP:B13N20.40  
A:Experimental source: BAC clone B13N20; strain OR74A  
C:Genetics:  
A:Gene: NCSP:B13N20.40  
A:Map position: 6

Query Match 10.5%; Score 64; DB 2; Length 108;  
Best Local Similarity 32.9%; Pred. No. 33;  
Matches 28; Conservative 7; Mismatches 34; Indels 16; Gaps 4;

QY	13	LVLGILWLA	-----LRSVAGEQAPGTA-PCSRGSSWSADLDKCMDCASCARPHSDFLC 65
Db	30	LRLRLWLLTRRREMSLRMSLYPKGGGLPFSKGTITTS	-----LVVLMAEPHSDCL 82
QY	66	--GCAAAPPPFRLIWPILGGALS	88
Db	83	PTGLRARSQESHLDPITQAALDL	107

RESULT 2

T29620  
hypothetical protein R10A10.2 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T29620  
R:Wamsley, P.; Bradshaw, H.  
A:Description: The sequence of C. elegans cosmid R10A10.  
A:Reference number: Z20653  
A:Accession: T29620  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-112 <WAM>  
A:Cross-references: UNIPROT:P91404; EMBL:U80449; PIDN:AAB37826.1; GSPDB:GN00019; CESP:R1  
A:Experimental source: strain Bristol N2; clone R10A10  
C:Genetics:  
A:Gene: CESP:R10A10.2  
A:Map position: 1  
A:Introns: 17/2; 59/1

C:Superfamily: yeast hypothetical protein YOL133w; RING finger homology

Query Match 10.4%; Score 63; DB 2; Length 112;  
Best Local Similarity 27.5%; Pred. No. 42;  
Matches 19; Conservative 8; Mismatches 22; Indels 20; Gaps 3;

Qy 11 RLLVLGLLALLRSVAGSQAPGTPCPSRGSSWSADLDKCMDCASCRRARPHSDFCIGCAAA 70

Db 28 RPFVLKKKNAL-----AVWAMDVE-CDTCAICRVHLMEE-CLRCQSE 67

Qy 71 PPAPFRLW 79

Db 68 PSAECYVW 76

RESULT 3

FEPE

C:Species: Peptostreptococcus asaccharolyticus

C:Keywords: Non-heme iron proteins. IX. The amino acid sequence of ferredoxin from Micrococcus

C:Date: 24-Apr-1984 #sequence\_revision 23-Mar-1995 #text\_change 12-Jul-2004

C:Accession: A00196

R:Tsunoda, J.N.; Yasunobu, K.T.; Whiteley, H.R.

J. Biol. Chem. 243, 6262-6272, 1968

A:Title: Non-heme iron proteins. IX. The amino acid sequence of ferredoxin from Micrococcus

A:Reference number: A92040; MUID:69054261; PMID:5723466

A:Note: the source is designated as Micrococcus aerogenes

A:Accession: A00196

A:Molecule type: protein

A:Residues: 1-21,23-24,'Q',26-55 <TSU>

A:Cross-references: UNIPROT:P00193

R:Backes, G.; Mino, Y.; Loehr, T.M.; Meyer, T.E.; Cusanovich, M.A.; Sweeney, W.V.; Adman

J. Am. Chem. Soc. 113, 2055-2064, 1991

A:Title: The environment of Fe4S4 clusters in ferredoxins and high-potential iron protein

A:Reference number: A44688

A:Contents: annotation; X-ray crystallography, 2.0 angstroms; sequence revision

A:Note: sequence correction confirmed by peptide sequencing

R:Adman, E.T.; Sieker, L.C.; Jensen, L.H.

submitted to the Brookhaven Protein Data Bank, August 1976

A:Reference number: A50836; PDB:1FDX

A:Contents: annotation; X-ray crystallography, 2.0 angstroms, residues 1-21,'I',23-24,26

R:Adman, E.T.; Sieker, L.C.; Jensen, L.H.

J. Biol. Chem. 251, 3801-3806, 1976

A:Title: Structure of Peptococcus aerogenes ferredoxin. Refinement at 2 angstroms resolution

A:Reference number: A92192; MUID:76213238; PMID:932007

A:Contents: annotation; X-ray crystallography, 2.0 angstroms

R:Adman, E.T.; Sieker, L.C.; Jensen, L.H.

J. Biol. Chem. 248, 3987-3996, 1973

A:Title: The structure of a bacterial ferredoxin.

A:Reference number: A92136; MUID:73187389; PMID:4708097

A:Contents: annotation; X-ray crystallography, 2.8 angstroms

C:Keywords: 4Fe-4S; electron transfer; iron-sulfur protein; metalloprotein

F:1-54/Domain: ferredoxin 2[4Fe-4S] homology <FER>

F:18,11,14,46/Binding site: 4Fe-4S cluster (Cys) (covalent) #status experimental

F:18,36,39,42/Binding site: 4Fe-4S cluster (Cys) (covalent) #status experimental

Query Match 10.0%; Score 61; DB 1; Length 55;

Best Local Similarity 33.3%; Pred. No. 37;

Matches 12; Conservative 4; Mismatches 12; Indels 8; Gaps 1;

Qy 39 GSSWSADLDKCMDCASCRRARPHSDFCIGCAAAPAP 74

Db 26 GSIWAIDADSDICDGCAS-----VCPVGADNP 53

RESULT 4

S58086

N:Allothionein 3 - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 13-Jan-1996 #sequence\_revision 19-Apr-1996 #text\_change 09-Jul-2004

C:Accession: S58086; I52636

R:Amoureux, M.C.; Rethaus, B.; Wurch, T.; Colpaert, F.C.; Pauwels, P.J.

submitted to the EMBL Data Library, July 1995

A:Reference number: S58084

A:Accession: S58086

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-66 <AMO>

A:Cross-references: UNIPROT:P37361; EMBL:X89603; NID:G908880; PIDN:CAA61762.1; PID:G9088

R:Kobayashi, H.; Uchida, Y.; Ihara, Y.; Nakajima, K.; Kohaaka, S.; Miyatake, T.; Tsuji,

Brain Res. Mol. Brain Res. 19, 188-194, 1993

A:Title: Molecular cloning of rat growth inhibitory factor cDNA and the expression in th

A:Reference number: I52636; MUID:94018480; PMID:8412560

A:Accession: I52636

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-66 <KOB>

A:Cross-references: GB:S65838; NID:G425381; PIDN:AAB28366.1; PID:G425382

C:Superfamily: metallothionein

C:Keywords: acetylated amino end; chelation; metal binding; metal-thiolate cluster

F:1/Modified site: acetylated amino end (Met) #status predicted

F:6,8,14,16,20,22,25,27,30/Binding site: transition metal ions (Cys) #status predicted

F:34,35,37,38,42,45,49,51,62,64,65/Binding site: transition metal ions (Cys) #status pre

Query Match 10.0%; Score 61; DB 2; Length 66;

Best Local Similarity 35.0%; Pred. No. 43;

Matches 14; Conservative 2; Mismatches 22; Indels 2; Gaps 2;

Qy 31 PGTAPCSRGSSWSADLDKCMDCASCRRARPHSDFCIGCAAA 70

Db 3 PETCPPTGGSGCTCS-DKC-KCKGCKTNCKKSCCCCPA 40

RESULT 5

167866

growth inhibitory factor - mouse

C:Species: Mus sp. (mouse)

C:Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 20-Aug-1999

C:Accession: I67866

R:Naruse, S.; Igarashi, S.; Furuya, T.; Kobayashi, H.; Miyatake, T.; Tsuji, S.

Gene 144, 283-287, 1994

A:Title: Structures of the human and mouse growth inhibitory factor-encoding genes.

A:Reference number: I53803; MUID:94314230; PMID:8039715

A:Accession: I67866

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-68 <RES>

A:Cross-references: GB:S72046; NID:G565191; PIDN:AAB31397.1; PID:G565192

C:Genetics:

A:Gene: GIF

A:Introns: 11/1; 33/1

C:Superfamily: metallothionein

Query Match 10.0%; Score 61; DB 2; Length 68;

Best Local Similarity 35.0%; Pred. No. 44;

Matches 14; Conservative 2; Mismatches 22; Indels 2; Gaps 2;

Qy 31 PGTAPCSRGSSWSADLDKCMDCASCRRARPHSDFCIGCAAA 70

Db 3 PETCPPTGGSGCTCS-DKC-KCKGCKTNCKKSCCCCPA 40

RESULT 6

A46034

metallothionein 3, brain-specific - mouse

N:Alternate names: neurotrophic growth inhibitory factor

C:Species: Mus musculus (house mouse)

C:Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004

C:Accession: A46034

R:Palmiter, R.D.; Findley, S.D.; Whitmore, T.E.; Durnam, D.M.

Proc. Natl. Acad. Sci. U.S.A. 89, 6333-6337, 1992

A:Title: MT-III, a brain-specific member of the metallothionein gene family.

A:Reference number: A46034; MUID:92335292; PMID:1631128

A:Accession: A46034

A:Status: preliminary

A:Molecule type: DNA

A;Residues: 1-68 <PAL>  
A;Cross-references: UNIPROT:P28184; GB:M93310; NID:g199133; PIDN:AAA39529.1; PID:g199134  
A;Note: sequence extracted from NCBI backbone (NCBIN:108715, NCBIN:111115, NCBIP:108716)  
C;Superfamily: metallothionein

Query Match 10.0%; Score 61; DB 2; Length 68;  
Best Local Similarity 35.0%; Pred. No. 44;  
Matches 14; Conservative 2; Mismatches 22; Indels 2; Gaps 2;

QY 31 PGTAPCSRSSWSADLDKMDKCDKACRCRAPHSDFCGLGCAA 70  
DB 3 PPTCPPTGSGTCS-DKC-KCKGCKCTNCKSCSCCPA 40

## RESULT 7

T03860  
TA20 protein - common tobacco  
C;Species: Nicotiana tabacum (common tobacco)  
C;Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
C;Accession: T03860  
R;Beale, T.P.; Goldberg, R.B.  
submitted to the EMBL Data Library, October 1996  
A;Description: Nicotiana tabacum gene expressed in anthr.  
A;Reference number: Z15122  
A;Accession: T03860  
A;Status: preliminary; translated from GB/EMBL/DBDJ  
A;Molecule type: DNA  
A;Residues: 1-76 <BEA>  
A;Cross-references: UNIPROT:Q24155; EMBL:U73164; NID:g1657813; PIDN:AB18190.1; PID:g1657813  
A;Experimental source: tissue-type anthr  
C;Genetics:  
A;Gene: TA20

Query Match 10.0%; Score 60.5; DB 2; Length 76;  
Best Local Similarity 40.0%; Pred. No. 54;  
Matches 12; Conservative 4; Mismatches 9; Indels 5; Gaps 1;

QY 40 SSWASDLKMDP-----CASCRCRAPHSDFC 64  
DB 27 SSVADGDSCTDHCAITCAFCNGKQYNYC 56

## RESULT 8

B46034  
metallothionein 3, brain-specific - human  
N;Alternate names: growth inhibitory factor; metallothionein WT-III  
C;Species: Homo sapiens (man)  
C;Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C;Accession: B46034; JH0463; S58084; I53803  
R;Palmiter, R.D.; Findley, S.D.; Whitmore, T.E.; Durnam, D.M.  
Proc. Natl. Acad. Sci. U.S.A. 89, 6333-6337, 1992  
A;Title: MT-III, a brain-specific member of the metallothionein gene family.  
A;Reference number: A46034; MUID:92335292; PMID:1631128  
A;Accession: B46034  
A;Molecule type: DNA  
A;Residues: 1-68 <PAL>  
A;Cross-references: UNIPROT:P25713; GB:M93311; NID:g187546; PIDN:AAA36214.1; PID:g187547  
A;Note: sequence extracted from NCBI backbone (NCBIN:108717, NCBIN:111117, NCBIP:108718)  
R;Tsuiji, S.; Kobayashi, H.; Uchida, Y.; Ihara, Y.; Miyatake, T.  
EMBO J. 11, 4843-4850, 1992  
A;Title: Molecular cloning of human growth inhibitory factor cDNA and its down-regulation  
A;Reference number: S28393; MUID:93099858; PMID:1464312  
A;Accession: S28393  
A;Molecule type: mRNA  
A;Residues: 1-68 <TSU>  
A;Cross-references: EMBL:D13365  
R;Uchida, Y.; Takio, K.; Titani, K.; Ihara, Y.; Tomonaga, M.  
Neuron 7, 337-347, 1991  
A;Title: The growth inhibitory factor that is deficient in the Alzheimer's disease brain  
A;Reference number: JH0463; MUID:91337462; PMID:1973033  
A;Accession: JH0463  
A;Molecule type: protein  
A;Residues: 1-68 <UCH>

A;Note: the amino end was shown to be blocked  
R;Amoureux, M.C.; Remhsaus, E.; Wurch, T.; Colpaert, F.C.; Pauwels, P.J.  
submitted to the EMBL Data Library, July 1995  
A;Reference number: S58084  
A;Accession: S58084  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-68 <AMO>  
A;Cross-references: EMBL:X89604; NID:g914850; PIDN:CAA61763.1; PID:g914851  
R;Naruse, S.; Igarashi, S.; Furuya, T.; Kobayashi, H.; Miyatake, T.; Tsuji, S.  
Gene 144, 283-287, 1994  
A;Title: Structures of the human and mouse growth inhibitory factor-encoding genes.  
A;Reference number: I53803; MUID:94314230; PMID:8039715  
A;Accession: I53803  
A;Status: preliminary; translated from GB/EMBL/DBDJ  
A;Molecule type: DNA  
A;Residues: 1-68 <RES>  
A;Cross-references: GB:S72043; NID:g565189; PIDN:AB31396.1; PID:g565190  
C;Genetics:  
A;Gene: GDB:MT3; GIF  
A;Cross-references: GDB:I34716; OMIM:139255  
A;Map position: 16q13-16q13  
A;Introns: 11/1; 33/1  
C;Superfamily: metallothionein  
C;Keywords: Alzheimer's disease; blocked amino end; brain

Query Match 9.7%; Score 59; DB 2; Length 68;  
Best Local Similarity 39.5%; Pred. No. 68;  
Matches 17; Conservative 1; Mismatches 17; Indels 8; Gaps 3;

QY 31 PGTAPC-SRGSWSADLDKC--MDCASCRCRAPHSDFCGLGCAA 70  
DB 3 PETCPSPGSGCTCADSCCKGCKTSCCKS-----CGSCCPA 40

## RESULT 9

E69969  
hypothetical protein yqzF - Bacillus subtilis  
C;Species: Bacillus subtilis  
C;Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
C;Accession: E69969  
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertea  
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch  
A.; Ehrlich, S.D.; Emmeron, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.  
Nature 390, 249-256, 1997  
A;Authors: Foulger, D.; Fritz, C.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallen  
ich, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hulio, M.F.  
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,  
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mausel  
Y., M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle  
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,  
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror  
Akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terptrak, P.; Tognoni, A.; Tosato, V.; Uchiyama  
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.  
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.  
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.  
A;Reference number: A69580; MUID:98044033; PMID:9384377  
A;Accession: E69969  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-78 <KUN>  
A;Cross-references: UNIPROT:Q32015; GB:Z99116; GB:AL009126; NID:g2634723; PIDN:CAB14342  
A;Experimental source: strain 168  
C;Genetics:  
A;Gene: yqzF

Query Match 9.6%; Score 58.5; DB 2; Length 78;  
Best Local Similarity 37.5%; Pred. No. 85;  
Matches 15; Conservative 10; Mismatches 12; Indels 3; Gaps 2;

QY 74 PRLWLPILGALSITFVLGL--LSGFLVWRRCRRSSP 111  
DB 35 PFSALW-LQGLSGFIFFAIGLYVLAGFITYLRDRKNQVSP 73



Db 17 LKLLTASLSSATSFSAGGMS-----SRPSSISPV--ALERSAARP-----ML 62  
QY 69 AAP--PAPRLWPILGGALSTFVLGLSLGFLVWRCHRRSSPP 112  
Db 63 ETFRKKVGR-LWMCFSKAWILPTILCMDRSP-----RTRASPP 100

RESULT 15  
G82702  
hypothetical protein XF1281 [imported] - Xylella fastidiosa (strain 9a5c)  
C:Species: Xylella fastidiosa  
C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004  
C:Accession: G82702  
R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequences  
Nature 406, 151-157, 2000  
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
A:Reference number: A82515; MUID:20365717; PMID:10910347  
A:Note: for a complete list of authors see reference number A59328 below  
A:Accession: G82702  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-67 <SIM>  
A:Cross-references: UNIPROT:Q9PD08; GB:AE003961; GB:AE003849; NID:g9106254; PIDN:AAF8409  
A:Experimental source: strain 9a5c  
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000  
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigh Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E. A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira M.; Tsuchiko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z A:Reference number: A59328  
A:Contents: annotation  
C:Genetics:  
A:Gene: XF1281

Query Match 9.3%; Score 56.5; DB 2; Length 67;  
Best Local Similarity 33.8%; Pred. No. 1.2e+02;  
Matches 22; Conservative 4; Mismatches 24; Indels 15; Gaps 4;  
QY 38 RGSWSADL-DKCMDCASCARPHSDFCIG----CAAAPPAPFRLLWPILGGALSLTFVL 92  
Db 10 RGYSWFNDRDCSAVRSCRYGVDLDVLSMRDQCCA-----LLNLVMS---SYLMVF 59  
QY 93 GLLSG 97  
Db 60 GSGSG 64

Search completed: February 14, 2005, 07:13:57  
Job time : 39 secs

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OM protein - protein search, using sw\_model

Run on: February 14, 2005, 06:56:46 ; Search time 174 Seconds  
(without alignments)  
335.500 Million cell updates/sec

Title: US-10-062-831-59  
Perfect score: 608  
Sequence: 1 MARGSLRLRLVGLMLA.....LSGFLVWRCRRSSPPPX 114

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 317667

Minimum DB seq length: 0  
Maximum DB seq length: 114

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	74.5	12.3	112	2 Q6ZB85	Q6ZB85 oryza sativ
2	73.5	12.1	81	1 PORD METTH	P56815 methanobact
3	67	11.0	83	2 Q82TF5	Q82TF5 pyrobaculum
4	67	11.0	90	2 Q7U455	Q7U455 synecococc
5	66	10.9	97	2 Q7N1L0	Q7N1L0 chromobacte
6	66	10.9	107	2 Q36605	Q36605 hepatitis e
7	66	10.9	107	2 Q36606	Q36606 hepatitis e
8	65	10.7	77	2 Q92MCI	Q92MCI rhizobium m
9	65	10.7	105	2 Q884Q0	Q884Q0 pseudomonas
10	64.5	10.6	112	1 PLA8 MOUSE	Q9J148 mus musculu
11	63.5	10.4	85	2 Q9P9E6	Q9P9E6 methanococc
12	63.5	10.4	85	2 Q6LX46	Q6LX46 methanococc
13	63.5	10.4	90	2 Q6N8D2	Q6N8D2 rhodospseud
14	63	10.4	82	2 Q6ZGY2	Q6ZGY2 oryza sativ
15	63	10.4	112	2 P91404	P91404 caenorhabdi
16	62.5	10.3	56	2 Q7MUS0	Q7MUS0 porphyromon
17	62	10.2	54	1 FER PEPAS	P00193 peptostrept
18	62	10.2	91	2 Q70LU6	Q70LU6 mus musculu
19	62	10.2	98	2 Q6CCG4	Q6CCG4 yarowia li
20	62	10.2	114	2 Q6Z6H1	Q6Z6H1 oryza sativ
21	61.5	10.1	75	2 Q7QX99	Q7QX99 giardia lam
22	61.5	10.1	84	2 Q65HK2	Q65HK2 bacillus li
23	61	10.0	66	1 MT3 RAT	P37361 rattus norv
24	61	10.0	68	1 MT3 MOUSE	P28184 mus musculu
25	61	10.0	70	2 Q82PP8	Q82PP8 streptomyce
26	60.5	10.0	76	2 Q24155	Q24155 nicotiana t
27	60.5	10.0	89	2 Q8TZ58	Q8TZ58 methanopyru
28	60.5	10.0	101	2 Q9AX16	Q9AX16 oryza sativ
29	60	9.9	94	2 Q68VL6	Q68VL6 azoarcus sp
30	60	9.9	100	2 Q7VBB2	Q7VBB2 prochloroco
31	59.5	9.8	58	2 Q68GX9	Q68GX9 canis lupus

32	59.5	9.8	58	2 Q68GY0	Q68GY0 canis latra
33	59.5	9.8	100	1 TXOB ATRIL	Q9bjv7 atrax sp. i
34	59.5	9.8	112	2 Q7X5Y1	Q7X5Y1 oryza sativ
35	59	9.7	59	2 Q9W7U2	Q9W7U2 hepatitis e
36	59	9.7	68	1 MT3_HUMAN	P25713 homo sapien
37	59	9.7	78	2 Q7QV05	Q7QV05 giardia lam
38	59	9.7	92	2 Q729E3	Q729E3 desulfovibr
39	59	9.7	94	2 Q8VUF9	Q8VUF9 azoarcus ev
40	59	9.7	109	2 Q7PNW0	Q7PNW0 anopheles g
41	58.5	9.6	58	2 Q8JUL4	Q8JUL4 hepatitis e
42	58.5	9.6	78	1 YQZP_BACSU	O32015 bacillus su
43	58.5	9.6	95	2 Q84QH9	Q84QH9 triticum ae
44	58.5	9.6	106	2 Q6YX12	Q6YX12 oryza sativ
45	58.5	9.6	107	2 Q8TYE4	Q8TYE4 methanopyru

ALIGNMENTS

RESULT 1

Q6ZB85	PRELIMINARY;	PRT;	112 AA.
ID Q6ZB85			
AC Q6ZB85;			
DT 05-JUL-2004 (Tremblrel. 27, Created)			
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)			
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)			
DE Hypothetical protein OJ1113_A10.29.			
GN Name=OJ1113_A10.29;			
OS Oryza sativa (japonica cultivar-group).			
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;			
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;			
OC Ehrhartoideae; Oryzae; Oryza.			
OX NCBI_TaxID=39947;			
RN [1]			
RP SEQUENCE FROM N.A.			
RA Sasaki T., Matsumoto T., Yamamoto K.;			
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 8, BAC			
RT clone:OJ1113_A10.29;"			
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.			
DR EMBL; AP004643; BAD09755.1; -.			
KW Hypothetical protein.			
SQ SEQUENCE 112 AA; 12726 MW; A900C5AF329E2973 CRC64;			

Query Match	12.3%;	Score 74.5;	DB 2;	Length 112;
Best Local Similarity	34.5%;	Pred. No. 17;		
Matches	20;	Conservative	8;	Mismatches
			17;	Indels
			13;	Gaps
			3;	
QY	59	PHSD--FCLGCAAPAPFRLLMFILGGAUSLTFTVLGSLGFLVWRCRRSSPPPX	114	
Db	3	PHSDSIFLLGAAHQPRP-----PVVSNALT-----KLEMMVAPRRRKQRCPPQP	49	

RESULT 2

PORD METTH	STANDARD;	PRT;	81 AA.
ID PORD METTH			
AC P56815;			
DT 30-MAY-2000 (Rel. 39, Created)			
DT 30-MAY-2000 (Rel. 39, Last sequence update)			
DT 25-OCT-2004 (Rel. 45, Last annotation update)			
DE Pyruvate synthase subunit pord (EC 1.2.7.1) (Pyruvate oxidoreductase			
DE delta chain) (POR) (Pyruvic-ferredoxin oxidoreductase delta subunit).			
GN Name=pord; OrderedLocusNames=MT1740.1;			
OS Methanobacterium thermoautotrophicum.			
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;			
OC Methanobacteriaceae; Methanothermobacter.			
OX NCBI_TaxID=187420;			
RN [1]			
RP SEQUENCE FROM N.A.			
RA STRAIN=Delta H;			
RA MEDLINE=98037514; PubMed=9371463;			
RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,			
RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,			
RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,			

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RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
RA Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
RA McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
RT "Complete genome sequence of Methanobacterium thermoautotrophicum
RL J. Bacteriol. 179:7135-7155(1997).";
CC -|- CATALYTIC ACTIVITY: Pyruvate + CoA + oxidized ferredoxin = acetyl-
CC CoA + CO(2) + reduced ferredoxin.
CC -|- COFACTOR: Binds 2 4Fe-4S clusters.
CC -|- SUBUNIT: Heterotetramer of one alpha, one beta, one delta and one
CC gamma chain.
CC -|- SIMILARITY: Contains 2 4Fe-4S type ferredoxin domains.
CC -|- CAUTION: There seems to be a sequencing error that fuses together
CC porc and pord. We have cut the ORF into its two constituents.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.ebi.ac.uk/announcements/
CC or send an email to license@ebi.ac.uk).
CC -----
DR EMBL; AE000929; AAB86210.1; ALT_INIT.
DR HSPF; P00195; 1CLF.
DR InterPro; IPR001450; 4Fe4S_ferredoxin.
DR Pfam; PF00037; Fer4; 2.
DR PROSITE; PR00353; 4FE4S_FERREDOXIN.
DR PROSITE; PS00198; 4FE4S_FERREDOXIN; 2.
KW 4Fe-4S; Complete proteome; Electron transport; Iron-sulfur;
KW Oxidoreductase; Repeat.
FT METAL 34 34 Iron-sulfur 1 (4Fe-4S) (Potential).
FT METAL 37 37 Iron-sulfur 1 (4Fe-4S) (Potential).
FT METAL 40 40 Iron-sulfur 1 (4Fe-4S) (Potential).
FT METAL 44 44 Iron-sulfur 2 (4Fe-4S) (Potential).
FT METAL 60 60 Iron-sulfur 2 (4Fe-4S) (Potential).
FT METAL 63 63 Iron-sulfur 2 (4Fe-4S) (Potential).
FT METAL 66 66 Iron-sulfur 2 (4Fe-4S) (Potential).
FT METAL 70 70 Iron-sulfur 1 (4Fe-4S) (Potential).
SQ SEQUENCE 81 AA; 9121 MW; 219A9CCAE8A41604 CRC64;
Query Match 12.1%; Score 73.5; DB 1; Length 81;
Best Local Similarity 29.2%; Pred. No. 16;
Matches 19; Conservative 8; Mismatches 21; Indels 17; Gaps 4;
QY 31 PGTAFCPSRGSSWSA-----DLDKMDCASCRA-----RPHS---DFCLGCA-AAPPA 73
DB 11 PGSTVKNKTGSRWTFKPKVLDKDKICDCNCLFCPEGCINREHEIDYDYCKGCGICAEKC 70
QY 74 PFRLL 78
DB 71 PVKAI 75
RESULT 3
Q8ZTF5 Q8ZTF5 PRELIMINARY; PRT; 83 AA.
AC Q8ZTF5;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE 2-ketoacid ferredoxin oxidoreductase delta subunit.
GN OrderedLocustNames=PAE3276;
OS Pyrobaculum aerophilum.
OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
OC Theomproteaceae; Pyrobaculum.
OX NCBI_TaxID=13773;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=IM2;
RX MEDLINE=21664397; PubMed=11792869; DOI=10.1073/pnas.241636498;
RA Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
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RA Miller J.H.;
RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
RT aerophilum.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
DR EMBL; AE009922; AAL64806.1; -.
DR HSPF; P00193; 1DUR.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0005506; P:iron ion binding; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR Pfam; PF00037; Fer4; 2.
DR PRINTS; PR00353; 4FE4S_FERREDOXIN.
DR PROSITE; PS00198; 4FE4S_FERREDOXIN; 2.
KW 4Fe-4S; Complete proteome; Iron-sulfur; Metal-binding.
SQ SEQUENCE 83 AA; 8999 MW; 11EE9466C4807A37 CRC64;
Query Match 11.0%; Score 67; DB 2; Length 83;
Best Local Similarity 30.4%; Pred. No. 66;
Matches 17; Conservative 4; Mismatches 13; Indels 22; Gaps 3;
QY 34 APCSRG--SSWS-----ADLDKMDASC-----RAPHSDPCLGC 67
DB 8 APASAGITGTRTYKYPVNLSKCIDCGLCWLYCPESVIDWEKGTGVKVIDYDFCKGC 63
RESULT 4
Q7U455 Q7U455 PRELIMINARY; PRT; 90 AA.
AC Q7U455;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein precursor.
DE OrderedLocustNames=SYNW2217;
GN Synchococcus sp. (strain WH8102).
OS Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX NCBI_TaxID=84588;
RN [1];
RP SEQUENCE FROM N.A.
RX MEDLINE=22825697; PubMed=12917641; DOI=10.1038/nature01943;
RA Palenik B., Brahmsha B., Larimer F.W., Land M.L., Hauser L.,
RA Chain P., Lamerdin J.E., Regalia W., Allen E.E., McCarren J.,
RA Paulsen I.T., Dufresne A., Partensky F., Webb E.A., Waterbury J.;
RT "The genome of a motile marine Synechococcus.";
RL Nature 424:1037-1042(2003).
DR EMBL; BX569695; CA808732.1; -.
KW Complete proteome; Hypothetical protein; Signal.
FT SIGNAL 1 37 Potential.
SQ SEQUENCE 90 AA; 10051 MW; 82FAA501C7C64958 CRC64;
Query Match 11.0%; Score 67; DB 2; Length 90;
Best Local Similarity 27.8%; Pred. No. 71;
Matches 30; Conservative 12; Mismatches 32; Indels 34; Gaps 4;
QY 7 RRLRLVLVLGWLALLRSVAGEQAPGTPAPCSRGSSWSADLDKMDASCARPHSDPCLG 66
DB 11 RWLDRLMLNLVVLILG--AGFFGVAVAAQTQGRSALMDL----- 48
QY 67 CAAPAPPAPFLLW--PILGGALSLTFVLGSLSGFLVW---RRCRRERS 110
DB 49 -----FOALWQPLFTPAISLLIMALLSGILSWQRRVLKTRDS 88
RESULT 5
Q7NTL0 Q7NTL0 PRELIMINARY; PRT; 97 AA.
AC Q7NTL0;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=CV3044;
OS Chromobacterium violaceum.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
```



OC Neisseriaceae; Chromobacterium.  
RN NCBI\_TaxID=536;  
OX [1]  
PC STRAIN=A7CC 12472 / DSM 30191;  
RC MEDLINE=22892880; PubMed=14500782; DOI=10.1073/pnas.1832124100;  
RX Vasconcelos A.T.R., de Almeida D.F., Hungria M., Guimaraes C.T.,  
RA Antonio R.V., Almeida F.C., de Almeida L.G.P., de Almeida R.,  
RA Alves-Gomes J.A., Arade E.M., Araribe J., de Araujo M.F.F.,  
RA Atolfi-Filho S., Azevedo V., Baptista A.J., Bataus L.A.M.,  
RA Batista J.S., Belo A., van den Berg C., Bogo M., Bonatto S.,  
RA Bordignon J., Brigidio M.M., Brito C.A., Brocchi M., Burley H.A.,  
RA Canargo A.A., Cardoso D.D.P., Carneiro N.P., Carraro D.M.,  
RA Carvalho C.M.B., Cascado J.C.M., Cavada B.S., Chueire L.M.O.,  
RA Crezynski-Pasa T.B., Cunha-Junior N.C., Fagundes N., Faicao C.L.,  
RA Fantinatti F., Farias I.P., Felipe M.S.S., Ferrari L.P., Ferro J.A.,  
RA Ferro M.I.T., Franco G.R., Freitas N.S.A., Furian L.R.,  
RA Gazzinelli R.T., Gomes E.A., Goncalves P.R., Grangeiro T.B.,  
RA Grattapaglia D., Grisard E.C., Hanna E.S., Jardim S.N., Laurino J.,  
RA Leoi L.C.T., Lima L.F.A., Loureiro M.F., Lyra M.C.C.P.,  
RA Madeira H.M.F., Manfio G.P., Maranhao A.Q., Martins W.S.,  
RA di Mauro S.M.Z., de Medeiros S.R.B., Meisner R.V., Moreira M.A.M.,  
RA Nascimento F.F., Nicolas M.F., Oliveira J.G., Oliveira S.C.,  
RA Paixao R.F.C., Parente J.A., Pedrosa F.O., Pena S.D.J., Pereira J.O.,  
RA Ramalho-Neto C.E., Reis A.M.M., Rigo L.U., Rondinelli E.,  
RA Santos E.B.P., Santos F.R., Schneider M.P.C., Seauanez H.N.,  
RA Silva A.M.R., da Silva A.L.C., Silva D.W., Silva R., Simoes I.C.,  
RA Simon D., Soares C.M.A., Soares R.B.A., Souza E.M., Souza K.R.L.,  
RA Souza R.C., Steffens M.B.R., Steindel M., Teixeira S.R., Urmenyi T.,  
RA Vetore A., Wassem R., Zaha A., Simpson A.J.G.;  
RT "The complete genome sequence of Chromobacterium violaceum reveals  
RT remarkable and exploitable bacterial adaptability."  
RL Proc. Natl. Acad. Sci. U.S.A. 100:11660-11665(2003).  
DR ENBL: AE016920: AAP060713.1; -;  
KW Complete proteome; Hypothetical protein.  
SQ SEQUENCE 97 AA; 10929 MW; FALEFEFB8B7DB7D CRC64;

Query Match 10.9%; Score 66; DB 2; Length 97;  
Best Local Similarity 25.2%; Pred. No. 95;  
Matches 29; Conservative 12; Mismatches 34; Indels 40; Gaps 3;

Oy 6 LRLLRLVGLWMLLRVSAGEQAPGTAPCSRGSSWSADLDKCMDCASCARPHSDFCFL 65  
:|||||:  
Db 1 MRYLRLVELALLLVAVTVQNHSVFELFFGQSWS-----38

Oy 66 GCACAAAPPRLWPILGGALSITFVLGLSLGVLMRRCRRE-----RSSPP 112  
:|||||:  
Db 39 ----APTIVELLUFFVVGAAG-----VGILLATFSYFKTRRLESOLKKELNRNRP 83

RESULT 6  
O36605 PRELIMINARY; PRT; 107 AA.

ID O36605  
AC O36605;  
DT 01-JAN-1998 (TREMBLrel. 05, Created)  
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE Strain Morocco/F23 ORF-1 (Fragment).

OS Hepatitis E virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;  
OC Hepevirus.  
OX NCBI\_TaxID=12461;  
RN [1]

SEQUENCE FROM N.A.  
RC STRAIN=Morocco/F23;  
RX MEDLINE=37475412; PubMed=9334924;  
RX DOI=10.1002/(SICI)1096-9071(199710)53:2<139::AID-JMW5>3.3.CO;2-O;  
RA Chatterjee R., Tsarev S., Pillot J., Coursaget P., Emerson S.U.,  
RA Purcell R.H.;  
RT "African strains of hepatitis E virus that are distinct from Asian  
RT strains.";  
RL J. Med. Virol. 53:139-144(1997).  
DR ENBL: AF010429; AAB66553.1; -;  
DR InterPro: IPRO09080; trnasy\_n\_ia\_bind.  
FT NON TER 1  
FT NON TER 107  
SQ SEQUENCE 107 AA; 10934 MW; 7P60EDCE2E56E7P8 CRC64;

Query Match 10.9%; Score 66; DB 2; Length 107;  
Best Local Similarity 27.2%; Pred. No. 1e+02;  
Matches 25; Conservative 8; Mismatches 27; Indels 32; Gaps 4;

Oy 35 PCSRGSSWSADLDKC-----MDCASCARPHSDFCLCACAAAPPAPFRLLWPIL 82  
:|||||:  
Db 20 PFSPGHVESANPFCESTLYTRTWSEVDASNAPOPD----IGLASEPPIPSRAAIPIL 75

Oy 83 GGALSITFVLGLSLGVLMRRCRERSPPPX 114  
:|||||:  
Db 76 AAPLP-----SIVPG-----PTPPPS 91

RESULT 7  
O36606 PRELIMINARY; PRT; 107 AA.

ID O36606;  
AC O36606;  
DT 01-JAN-1998 (TREMBLrel. 05, Created)  
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE Strain Morocco/F12 ORF-1 (Fragment).

OS Hepatitis E virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;  
OC Hepevirus.  
OX NCBI\_TaxID=12461;  
RN [1]

SEQUENCE FROM N.A.  
RC STRAIN=Morocco/F12;  
RX MEDLINE=97475412; PubMed=9334924;  
RX DOI=10.1002/(SICI)1096-9071(199710)53:2<139::AID-JMW5>3.3.CO;2-O;  
RA Chatterjee R., Tsarev S., Pillot J., Coursaget P., Emerson S.U.,  
RA Purcell R.H.;  
RT "African strains of hepatitis E virus that are distinct from Asian  
RT strains.";  
RL J. Med. Virol. 53:139-144(1997).

OC Neisseriaceae; Chromobacterium.  
RN NCBI\_TaxID=536;  
OX [1]  
PC STRAIN=A7CC 12472 / DSM 30191;  
RC MEDLINE=22892880; PubMed=14500782; DOI=10.1073/pnas.1832124100;  
RX Vasconcelos A.T.R., de Almeida D.F., Hungria M., Guimaraes C.T.,  
RA Antonio R.V., Almeida F.C., de Almeida L.G.P., de Almeida R.,  
RA Alves-Gomes J.A., Arade E.M., Araribe J., de Araujo M.F.F.,  
RA Atolfi-Filho S., Azevedo V., Baptista A.J., Bataus L.A.M.,  
RA Batista J.S., Belo A., van den Berg C., Bogo M., Bonatto S.,  
RA Bordignon J., Brigidio M.M., Brito C.A., Brocchi M., Burley H.A.,  
RA Canargo A.A., Cardoso D.D.P., Carneiro N.P., Carraro D.M.,  
RA Carvalho C.M.B., Cascado J.C.M., Cavada B.S., Chueire L.M.O.,  
RA Crezynski-Pasa T.B., Cunha-Junior N.C., Fagundes N., Faicao C.L.,  
RA Fantinatti F., Farias I.P., Felipe M.S.S., Ferrari L.P., Ferro J.A.,  
RA Ferro M.I.T., Franco G.R., Freitas N.S.A., Furian L.R.,  
RA Gazzinelli R.T., Gomes E.A., Goncalves P.R., Grangeiro T.B.,  
RA Grattapaglia D., Grisard E.C., Hanna E.S., Jardim S.N., Laurino J.,  
RA Leoi L.C.T., Lima L.F.A., Loureiro M.F., Lyra M.C.C.P.,  
RA Madeira H.M.F., Manfio G.P., Maranhao A.Q., Martins W.S.,  
RA di Mauro S.M.Z., de Medeiros S.R.B., Meisner R.V., Moreira M.A.M.,  
RA Nascimento F.F., Nicolas M.F., Oliveira J.G., Oliveira S.C.,  
RA Paixao R.F.C., Parente J.A., Pedrosa F.O., Pena S.D.J., Pereira J.O.,  
RA Ramalho-Neto C.E., Reis A.M.M., Rigo L.U., Rondinelli E.,  
RA Santos E.B.P., Santos F.R., Schneider M.P.C., Seauanez H.N.,  
RA Silva A.M.R., da Silva A.L.C., Silva D.W., Silva R., Simoes I.C.,  
RA Simon D., Soares C.M.A., Soares R.B.A., Souza E.M., Souza K.R.L.,  
RA Souza R.C., Steffens M.B.R., Steindel M., Teixeira S.R., Urmenyi T.,  
RA Vetore A., Wassem R., Zaha A., Simpson A.J.G.;  
RT "The complete genome sequence of Chromobacterium violaceum reveals  
RT remarkable and exploitable bacterial adaptability."  
RL Proc. Natl. Acad. Sci. U.S.A. 100:11660-11665(2003).  
DR ENBL: AE016920: AAP060713.1; -;  
KW Complete proteome; Hypothetical protein.  
SQ SEQUENCE 97 AA; 10929 MW; FAIEFEFB8B7DB7D CRC64;

Query Match 10.9%; Score 66; DB 2; Length 97;  
Best Local Similarity 25.2%; Pred. No. 95;  
Matches 29; Conservative 12; Mismatches 34; Indels 40; Gaps 3;

Oy 6 LRILLRVGLWMLLRVAGEQAPGTAPCSRGSSWSADLDKCMDCASCARPHSDFCFL 65  
:|||||:  
Db 1 MYLLRIVELALLLVAVTVQNHSVFELFFGQSWS-----38

Oy 66 GCACAAAPPRLWPILGGALSITFVLGLSLGVLMRRCRRE-----RSSPP 112  
:|||||:  
Db 39 ----APTIVELLUFFVVGAA-----VGLLATFSYFKTRRELSQLKKELNRNRP 83

RESULT 6  
O36605 PRELIMINARY; PRT; 107 AA.

ID O36605  
AC O36605;  
DT 01-JAN-1998 (TREMBLrel. 05, Created)  
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE Strain Morocco/F23 ORF-1 (Fragment).

OS Hepatitis E virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;  
OC Hepevirus.  
OX NCBI\_TaxID=12461;  
RN [1]

SEQUENCE FROM N.A.  
RC STRAIN=Morocco/F23;  
RX MEDLINE=37475412; PubMed=9334924;  
RX DOI=10.1002/(SICI)1096-9071(199710)53:2<139::AID-JMW5>3.3.CO;2-O;  
RA Chatterjee R., Tsarev S., Pillot J., Coursaget P., Emerson S.U.,  
RA Purcell R.H.;  
RT "African strains of hepatitis E virus that are distinct from Asian  
RT strains.";  
RL J. Med. Virol. 53:139-144(1997).  
DR ENBL: AF010429; AAB6553.1; -;  
DR InterPro: IPRO09080; trnasy\_n\_ia\_bind.  
FT NON TER 1  
FT NON TER 107  
SQ SEQUENCE 107 AA; 10934 MW; 7P60EDCE2E56E7P8 CRC64;

Query Match 10.9%; Score 66; DB 2; Length 107;  
Best Local Similarity 27.2%; Pred. No. 1e+02;  
Matches 25; Conservative 8; Mismatches 27; Indels 32; Gaps 4;

Oy 35 PCSRGSSWSADLDKC-----MDCASCARPHSDFCLCACAAAPPAPFRLLWPIL 82  
:|||||:  
Db 20 PFSPGHVESANPFCESTLYTRTWSEVDASNAQPDP----IGLASEPPIPSRAATPIL 75

Oy 83 GGALSITFVLGLSLGVLMRRCRERSPPPX 114  
:|||||:  
Db 76 AAPLP-----SIVPG-----PTPPPS 91

RESULT 7  
O36606 PRELIMINARY; PRT; 107 AA.

ID O36606;  
AC O36606;  
DT 01-JAN-1998 (TREMBLrel. 05, Created)  
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE Strain Morocco/F12 ORF-1 (Fragment).

OS Hepatitis E virus.  
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Hepeviridae;  
OC Hepevirus.  
OX NCBI\_TaxID=12461;  
RN [1]

SEQUENCE FROM N.A.  
RC STRAIN=Morocco/F12;  
RX MEDLINE=97475412; PubMed=9334924;  
RX DOI=10.1002/(SICI)1096-9071(199710)53:2<139::AID-JMW5>3.3.CO;2-O;  
RA Chatterjee R., Tsarev S., Pillot J., Coursaget P., Emerson S.U.,  
RA Purcell R.H.;  
RT "African strains of hepatitis E virus that are distinct from Asian  
RT strains.";  
RL J. Med. Virol. 53:139-144(1997).



SQ	SEQUENCE	85 AA; 9696 MW;	59DE68859B4EA718 CRC64;
	Query Match	10.4%; Score 63.5; DB 2; Length 85;	
	Best Local Similarity	25.0%; Pred. No. 1.Se+02;	
Matches	14; Conservative	8; Mismatches 15; Indels 19; Gaps	
QY	31 PGTAPCSRGGWSA-----DLDKMDCASC-----P-RARPHSDFCLGC 67   :: ::      :: : :	:	: :  :
DB	11 PGSSAKNTGSRVFKPVLPDQKVCRCENCYFCPEGCIQEXDGKFEDDYCKGC 66   :: ::      :: : :	:	: :~  :
RESULT 12			
Q6LX46	PRELIMINARY;	PRT;	85 AA.
ID AC Q6LX46;			
DT 05-JUL-2004 (TReMBLrel. 27, Created)			
DD 05-JUL-2004 (TReMBLrel. 27, Last sequence update)			
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)			
DN Pyruvate oxidoreductase (Synchase) subunit delta (SC 1.2.7.1).			
GE Name=porD; OrderedLocusNames=MWP1506;			
DN Methanococcus maripaludis.			
OC Archaea; Euryarchaeota; Methanococchi; Methanococcoales;			
OS Methanococcaceae; Methanococcus.			
OX NCBI_TaxID=39152;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN=S2 / LL;			
RA Hendrickson E.L., Kaul R., Zhou Y., Bovee D., Chapman P., Chung J., Conway de Macario E., Dodsworth J., Gillett W., Graham D.E., Haydock A.K., Kang A., Land M.L., Levy R., Lie T.J., Major T., Moore B., Porat I., Overbeek R., Palmeiri A., Rouse G., Saenphimmachak C., Soll D., Whitman W.B., Larimer F.W., Olson M.V., Leigh J.A.;			
RT "Complete genome sequence of the mesophilic hydrogenotrophic methanogen Methanococcus maripaludis".			
RL Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.			
RDR EMBL; BX957223; CAF31062.1; -; HSP; Q45560; 1BD6.			
DR GO; GO:0005489; P:electron transporter activity; IEA. GO; GO:0005506; P:iron ion binding; IEA. GO; GO:0019164; P:pyruvate synthase activity; IEA. GO; GO:0006118; P:electron transport; IEA. InterPro; IPRO01450; 4Fe4S ferredoxin. Pfam; PF00037; Fer4; 2. PRINTS; PR00353; 4FE4SFSDOXIN. PROSITE; PS00198; 4FE4S FERREDOXIN; 2. 4Fe-4S; Complete proteome; Iron:Iron-sulfur; Metal-binding.			
KW SQ SEQUENCE	85 AA; 9682 MW; 5D8B39859B4CD068 CRC64;		
	Query Match	10.4%; Score 63.5; DB 2; Length 85;	
	Best Local Similarity	25.0%; Pred. No. 1.Se+02;	
Matches	14; Conservative	8; Mismatches 15; Indels 19; Gaps	
QY	31 PGTAPCSRGGWSA-----DLDKMDCASC-----P-RARPHSDFCLGC 67   :: ::      :: : :	:	: :  :
Db	11 PGSSANNKTGSVRVKPVLPDQKVCRCENCYFCPEGCIQEXDGKFEDDYCKGC 66   :: ::      :: : :	:	: :~  :
RESULT 13			
Q6N8D2	PRELIMINARY;	PRT;	90 AA.
ID AC Q6N8D2;			
DT 05-JUL-2004 (TReMBLrel. 27, Created)			
DD 05-JUL-2004 (TReMBLrel. 27, Last sequence update)			
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)			
DE Hypothetical protein.			
GN OrderedLocusNames=RPA1971;			
OS Rhodopseudomonas palustris.			
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;			
OC Bradyrhizobiaceae; Rhodospirillum rubrum.			
OX NCBI_TaxID=1076;			
RN [1]			
RP SEQUENCE FROM N.A.			



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OM protein - protein search, using sw model

Run on: February 14, 2005, 06:47:40 ; Search time 163 Seconds  
(without alignments)  
270.495 Million cell updates/sec

Title: US-10-062-831-59  
Perfect score: 608  
Sequence: 1 MARGSLRLRLVGLWLA.....LSGFLVWRCRRRSSPPPX 114

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 1221546

Minimum DB seq length: 0  
Maximum DB seq length: 114

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	608	100.0	114	2	AAW73409 Human sec
2	337.5	55.5	94	7	ABU64233 Human CRY
3	274.5	45.1	112	3	AAV91463 Human sec
4	274.5	45.1	112	6	ADA57390 Human sec
5	274.5	45.1	112	7	ADC74462 Human sec
6	274.5	45.1	112	7	ADD38025 Human sec
7	274.5	45.1	112	8	ADL71535 Novel hum
8	191	31.4	32	6	ADA49370 Human Fnl
9	73.5	12.1	98	6	AAU66196 Propionib
10	73.5	12.1	98	6	ABM62715 Propionib
11	70	11.5	70	5	AAE22260 Human BAF
12	69	11.3	79	5	ABP06392 Human ORF
13	68.5	11.3	101	2	AAV74100 Human pro
14	68.5	11.3	114	4	AAU57190 Human sec
15	68.5	11.3	114	4	ABM53709 Propionib
16	68	11.2	70	5	AAE22254 Human BAF
17	68	11.2	70	5	AAE22263 Human BAF
18	68	11.2	112	7	ABO72961 Pseudomon
19	67.5	11.1	74	4	AAU47590 Propionib
20	67.5	11.1	74	4	ABM44109 Propionib
21	67	11.0	70	5	AAE22259 Human BAF
22	67	11.0	74	2	AAV31398 HEV pepti
23	67	11.0	111	4	AAU42650 Propionib
24	67	11.0	111	6	ABM39169 Propionib
25	66	10.9	70	5	AAE22261 Human BAF

26	66	10.9	70	5	AAE22252 Human BAF
27	65	10.7	70	5	AAE22255 Human BAF
28	65	10.7	70	5	AAE22257 Human BAF
29	65	10.7	70	5	AAE22265 Human BAF
30	65	10.7	70	5	AAE22264 Human BAF
31	65	10.7	87	8	ABO54761 Human gen
32	65	10.7	92	8	ADP29374 Human sec
33	64.5	10.6	61	4	AAU53825 Propionib
34	64.5	10.6	61	6	ABM50344 Propionib
35	64.5	10.6	112	8	ADJ76375 Marker ge
36	64.5	10.6	112	8	ADN43102 Amino aci
37	64.5	10.6	112	8	ADP74023 Murine on
38	64	10.5	65	8	ABO57703 Human gen
39	64	10.5	77	2	AAV12612 Human 5'
40	64	10.5	95	7	ABO67894 Pseudomon
41	64	10.5	100	4	AAE04262 Human gen
42	63.5	10.4	78	4	AAU58568 Propionib
43	63.5	10.4	78	6	ABM55087 Propionib
44	63	10.4	70	5	AAE22253 Human BAF
45	63	10.4	70	5	AAE22262 Human BAF

## ALIGNMENTS

RESULT 1  
AAW73409  
ID AAW73409 standard; protein; 114 AA.  
XX  
AC AAW73409;  
XX  
DT 19-FEB-1999 (first entry)  
XX  
DE Human secreted protein encoded by Gene No. 13.  
XX  
KW Secreted protein; human; protein therapy; gene therapy; blood disorder;  
KW pathological condition; diagnosis; cancer; neurological disorder;  
KW developmental abnormality; foetal deficiency; leukaemia; hepatic disease;  
KW immune system disorder; Alzheimer's disease; cognitive disorder;  
KW schizophrenia; prostate disease; autoimmune disorder; AIDS.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 114  
FT /note= "unspecified amino acid"  
XX  
PN WO9854206-A1.  
XX  
PD 03-DEC-1998.  
XX  
PP 28-MAY-1998; 98WO-US010868.  
XX  
PR 30-MAY-1997; 97US-0044039P.  
PR 30-MAY-1997; 97US-0048093P.  
PR 30-MAY-1997; 97US-0048101P.  
PR 30-MAY-1997; 97US-0048190P.  
PR 30-MAY-1997; 97US-0048356P.  
PR 30-MAY-1997; 97US-0050935P.  
PR 29-AUG-1997; 97US-0056250P.  
PR 29-AUG-1997; 97US-0056293P.  
PR 29-AUG-1997; 97US-0056296P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Ruben SM, Rosen CA, Carter KC, Dillon PJ, Endress GA, Yu G;  
PI Ni J, Feng P;  
XX  
DR WPI; 1999-070209/06.  
DR N-PSDB; AAV08823.  
XX  
PT New isolated human genes - useful for diagnosis and treatment of, e.g.  
PT cancers, neurological disorders, immune diseases, developmental disorders

or blood disorders.

Claim 11; Page 153; 189pp; English.

This sequence is encoded by a cDNA of the invention, designated Gene No. 13. This sequence represents a human secreted protein, and is expressed in keratinocytes and to a lesser extent in endothelial cells and placenta. The DNA sequences of the invention and their corresponding secreted polypeptides are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the DNA sequences. Specific uses are described for each of the DNA sequences and the encoded proteins, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, neurological disorders, developmental abnormalities and foetal deficiencies, blood disorders, leukaemias, diseases of the immune system (including allergies or asthma), hepatic diseases, Alzheimer's and cognitive disorders, schizophrenia, prostate diseases, autoimmune disorders and AIDS. The polypeptides are also useful for identifying their binding partners

Sequence 114 AA;

Query Match 100.0%; Score 608; DB 2; Length 114;  
Best Local Similarity 100.0%; Pred. No. 2.6e-55;  
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARGSLRLLRLVGLWLLALLRSVAGQAPGTAPCSRGSWSADLDKCMDCASCRRAPH 60  
Db 1 MARGSLRLLRLVGLWLLALLRSVAGQAPGTAPCSRGSWSADLDKCMDCASCRRAPH 60

Qy 61 SDFCLGCAAAPAPPRLLWLPILGGALSLTFVLGLLGLVWRCRRRSSPPPX 114  
Db 61 SDFCLGCAAAPAPPRLLWLPILGGALSLTFVLGLLGLVWRCRRRSSPPPX 114

RESULT 2  
ABU64233  
ID ABU64233 standard; protein; 94 AA.  
AC ABU64233;  
XX  
XX  
XX 11-MAR-2004 (first entry)  
XX Human CRYPTIC protein.  
XX Metabolic disorder; TNF receptor family member; FRADJ; CRYPTIC; agonist;  
XX antagonist; gene therapy; vaccine; anorectic; cytostatic; anti-HIV;  
XX antiinflammatory; cardiant; ophthalmological; neuroprotective;  
XX nephrotropic; antidiabetic; antiarteriosclerotic; hypotensive;  
XX antilipemic; weight loss; obesity; diabetes.  
XX Homo sapiens.  
XX WO2003077939-A1.  
XX  
XX 25-SEP-2003.  
XX  
XX 17-MAR-2003; 2003WO-EP050066.  
XX  
XX 19-MAY-2002; 2002US-0365851P.  
XX  
XX 14-MAY-2002; 2002US-0380565P.  
XX  
XX (GEST ) GENSET SA.  
XX  
XX Dialynas D, Lucas J, Scalia A;  
XX WPI; 2003-779086/73.  
XX N-PSDB; AAL56187.  
XX  
XX Use of FRADJ or CRYPTIC polypeptide for preparing a medicament for  
PT treating or preventing a disorder associated with excessive weight loss

or an obesity-related disorder.

Claim 2; Page 201; 206pp; English.

The present invention provides the human FRADJ and CRYPTIC proteins. These can be used in screening for antagonists or agonists of APM1 polypeptide or polypeptide fragment activity, comprising lipid partitioning, lipid metabolism or insulin-like activity. The agonist or antagonist of FRADJ or CRYPTIC is useful for preparing a medicament for treating or preventing a disorder associated with excessive weight loss, comprising cachexia, cancer-related weight loss, AIDS-related weight loss, chronic inflammatory disease-related weight loss, bulimia or anorexia, or an obesity-related disorder, comprising obesity, insulin resistance, atherosclerosis, atheromatous disease, heart disease, hypertension, stroke, syndrome X, insulin or non-insulin dependent diabetes mellitus, hyperlipidaemia, hyperuricaemia or diabetes-related complications, e.g., microangiopathic lesions, ocular lesions, retinopathy, neuropathy or renal lesions. The present sequence is a polypeptide shown in the exemplification of the invention

Sequence 94 AA;

Query Match 55.5%; Score 337.5; DB 7; Length 94;  
Best Local Similarity 63.2%; Pred. No. 2.9e-27;  
Matches 72; Conservative 1; Mismatches 6; Indels 35; Gaps 1;

Qy 1 MARGSLRLLRLVGLWLLALLRSVAGQAPGTAPCSRGSWSADLDKCMDCASCRRAPH 60  
Db 1 MARGSLRLLRLVGLWLLALLRSVAGQAPGTAPCSRGSWSADLDKCMDCASCRRAPH 60

Qy 61 SDFCLGCAAAPAPPRLLWLPILGGALSLTFVLGLLGLVWRCRRRSSPPPX 114  
Db 33 -----AAPPAPPRLLWLPILGGALSLTFVLGLLGLVWRCRRREKFTPI 79

RESULT 3  
AA91463  
ID AA91463 standard; protein; 112 AA.  
XX  
XX AC AA91463;  
XX  
XX 29-JUN-2000 (first entry)  
XX Human secreted protein sequence encoded by gene 13 SEQ ID NO:136.  
XX Human; secreted protein; diagnosis; cytostatic; immunosuppressive;  
XX antiHIV; antiinflammatory; nootropic; neuroprotective; antiallergic;  
XX osteopathic; antiarthritic; antibacterial; antidiabetic; antisthma;  
XX antipertotic; cardiant; gene therapy; cancer; neurological disorder;  
XX immune disease; inflammation; blood disorder; tumour; chromosome 16.  
XX Homo sapiens.  
XX WO200006698-A1.  
XX  
XX 10-FEB-2000.  
XX  
XX 29-JUL-1999; 99WO-US017130.  
XX  
XX 30-JUL-1998; 98US-0094657P.  
XX 05-AUG-1998; 98US-0095486P.  
XX 06-AUG-1998; 98US-0095454P.  
XX 06-AUG-1998; 98US-0095455P.  
XX 12-AUG-1998; 98US-0096319P.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX Komatsoulis GA, Rosen CA, Ruben SM, Duan R, Moore PA, Shi Y;  
XX Lafleur D, Wei Y, Ni J, Florence KA, Young PE, Brewer LA;  
XX Soppet DR, Endress GA, Ebner R, Olsen HS, Mucenski M;  
XX WPI; 2000-195282/17.  
XX N-PSDB; AAA26358.

XX New isolated human genes and the secreted polypeptides they encode,  
PT useful for diagnosis and treatment of e.g. cancers, neurological  
PT disorders, immune diseases, inflammation or blood disorders.  
XX  
PS Claim 11; Page 465; 634pp; English.  
XX  
CC The polynucleotide sequences given in AAA26346 to AAA26458 encode the  
CC human secreted proteins given in AAY91451 to AAY91491. The human secreted  
CC proteins can have activities based on the tissues and cells they are  
CC expressed in. Examples of the activities are: cytostatic;  
CC immunosuppressive; antiHIV; antiinflammatory; neurotropic; neuroprotective;  
CC antiallergic; osteoprotective; antidiabetic; antibacterial; antidiabetic;  
CC antiasthma; antipsoriatic; and cardiant. The polynucleotides and their  
CC corresponding secreted proteins are useful for preventing, treating or  
CC ameliorating medical conditions, e.g. by protein or gene therapy. Also  
CC pathological conditions can be diagnosed by determining the amount of the  
CC proteins in a sample or by determining the presence of mutations in the  
CC polynucleotides. Specific uses are described for each of the  
CC polynucleotides, based on which tissues they are most highly expressed  
CC in, and include developing products for the diagnosis or treatment of  
CC cancer, tumours, neurodegenerative disorders, developmental abnormalities  
CC and foetal deficiencies, blood disorders, diseases of the immune system,  
CC autoimmune diseases, hepatic and renal disease, inflammation, allergies,  
CC Alzheimer's and behavioural disorders, schizophrenia, osteoporosis,  
CC arthritis, infections, AIDS, spinal cord injuries, transplant rejection,  
CC diabetes, asthma, sepsis, acne, psoriasis, cardiovascular disorders,  
CC reproductive disorders, gastrointestinal disorders, respiratory disorders  
CC and metabolic disorders. The proteins or polynucleotides can also be used  
CC as food additives or preservatives. The proteins are also useful for  
CC identifying their binding partners. AAA26337 to AAA26345 and AAY91450 are  
CC sequences used in the exemplification of the present invention  
XX  
SQ Sequence 112 AA;  
Query Match 45.1%; Score 274.5; DB 3; Length 112;  
Best Local Similarity 96.4%; Pred. No. 1.2e-20;  
Matches 54; Conservative 1; Mismatches 0; Indels 1; Gaps 1;  
QY 1 MARGSLRRLRLVLLGLWLLALLRSVAGQAPGTCPSRGSSWSADLDKMDCA-SC 55  
DB 1 MARGSLRRLRLVLLGLWLLALLRSVAGQAPGTCPSRGSSWSADLDKMDCTSC 56  
RESULT 4  
ADA57390  
ID ADA57390 standard; protein; 112 AA.  
XX  
AC ADA57390;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Human secreted protein #172.  
XX  
XX immunosuppressive; antiinflammatory; antiasthmatic; antiallergic;  
KW cytostatic; cerebroprotective; neuroprotective; neurotropic;  
KW cardiovascular; antiarteriosclerotic; gene therapy;  
KW human secreted protein; immune disorder; inflammation;  
KW respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;  
KW inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;  
KW multiple sclerosis; ischaemic brain injury; Parkinson's disease;  
KW Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;  
KW triple helix formation; antisense gene therapy; forensic biology.  
XX  
OS Homo sapiens.  
XX  
PN WO2002102994-A2.  
XX  
PD 27-DEC-2002.  
XX  
PF 19-MAR-2002; 2002WO-US008278.  
XX  
PR 21-MAR-2001; 2001US-0277340P.

PR 19-JUL-2001; 2001US-0306171P.  
PR 13-NOV-2001; 2001US-0331287P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Rosen CA, Ruben SM;  
XX  
DR WPI; 2003-167512/16.  
DR N-PSDB; ADA56496.  
XX  
PT New human secreted polypeptides and polynucleotides, useful for  
PT diagnosing, treating or preventing e.g. immune disorders, inflammatory  
PT conditions, respiratory disorders, cancers, CNS disorders, or  
PT neurodegenerative disorders.  
XX  
PS Claim 13; SEQ ID NO 1582; 1754pp; English.  
XX  
CC The invention relates to 592 new human secreted polypeptides useful for  
CC diagnosing, treating or preventing e.g. immune disorders, inflammatory  
CC conditions, respiratory disorders, cancers, CNS disorders, or  
CC neurodegenerative disorders, or polypeptides comprising an amino acid  
CC sequence at least 95% identical to the new sequences. The polypeptides,  
CC antibodies or antibody fragments that bind to the polypeptides, nucleic  
CC acids encoding the polypeptides, agonists or antagonists that binds to  
CC the polypeptide, are useful in preparing diagnostic or pharmaceutical  
CC compositions for diagnosing, treating or preventing an e.g. immune  
CC disorders, inflammatory conditions (e.g. inflammatory bowel disease,  
CC nephritis or Crohn's disease), respiratory disorders (e.g. asthma and  
CC allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders  
CC (e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative  
CC disorders (e.g. Parkinson's disease or Alzheimer's disease), and  
CC cardiovascular disorders (e.g. atherosclerosis or myocarditis). The  
CC polynucleotides are useful for chromosome identification, chromosome  
CC mapping, for controlling gene expression through triple helix formation  
CC or antisense DNA or RNA, in gene therapy, for identifying individuals  
CC from minute biological samples, in forensic biology, and as hybridization  
CC probes. The polypeptides are useful for as molecular weight markers on  
CC sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE)  
CC gels, to raise antibodies, for testing biological activities, and for  
CC treating or preventing neural disorders, immune system disorders,  
CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,  
CC renal, proliferative and/or cancerous diseases. This sequence corresponds  
CC to one of the polypeptide of the invention. Note: The sequence data for  
CC this patent did form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 112 AA;  
Query Match 45.1%; Score 274.5; DB 6; Length 112;  
Best Local Similarity 96.4%; Pred. No. 1.2e-20;  
Matches 54; Conservative 1; Mismatches 0; Indels 1; Gaps 1;  
QY 1 MARGSLRRLRLVLLGLWLLALLRSVAGQAPGTCPSRGSSWSADLDKMDCA-SC 55  
DB 1 MARGSLRRLRLVLLGLWLLALLRSVAGQAPGTCPSRGSSWSADLDKMDCTSC 56  
RESULT 5  
ADC74462  
ID ADC74462 standard; protein; 112 AA.  
XX  
AC ADC74462;  
XX  
DT 01-JAN-2004 (first entry)  
XX  
DE Human secreted protein - SEQ ID 1095.  
XX  
KW antianaemic; antirheumatic; antiarthritic; antiinflammatory; antithyroid;  
KW antidiabetic; immunosuppressive; dermatological; neurotropic;  
KW antiparkinsonian; neuroprotective; neurotropic; antibacterial; virucide;  
KW fungicide; antiparasitic; antiarteriosclerotic; vulnery; cytostatic;  
KW haemopoietic; haematologic; anaemia; autoimmune disorder;

KW rheumatoid arthritis; inflammation; Grave's disease; diabetes;  
KW systemic lupus erythematosus; glomerulonephritis; neurodegenerative;  
KW Parkinson's; Alzheimer's; wound; hyperproliferative; atherosclerosis;  
KW cancer; bacterial; viral; fungal; parasitic infection; gene therapy;  
KW human.  
XX  
OS Homo sapiens.  
XX  
XX WO2003038063-A2.  
FN  
XX  
XX 08-MAY-2003.  
PD  
XX  
XX 19-MAR-2002; 2002WO-US008277.  
PF  
XX  
XX 21-MAR-2001; 2001US-0277340P.  
PR  
XX 19-JUL-2001; 2001US-0306171P.  
PR  
XX 13-NOV-2001; 2001US-0331287P.  
PR  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
PA  
XX  
XX Rosen CA, Ruben SM;  
PI  
XX WPI; 2003-430516/40.  
DR  
XX N-PSDB; ADC73847.  
DR  
XX  
XX New human secreted polypeptide for diagnosing, preventing or treating  
PT hematopoietic or hematologic disorders (e.g. anemia), autoimmune  
PT disorders (e.g. diabetes) or hyperproliferative disorders (e.g. cancer or  
PT atherosclerosis).  
XX  
XX Claim 16; SEQ ID NO 1095; 2272pp; English.  
PS  
XX  
XX The invention relates to a novel human secreted polypeptide comprising a  
CC defined sequence given in the specification. The polypeptide, nucleic  
CC acid molecule, antibody, agonist or antagonist of the invention may be  
CC useful for preparing a composition for diagnosing or treating a  
CC haemopoietic or haematologic disorder such as anaemia, autoimmune  
CC disorders such as rheumatoid arthritis, inflammation, Grave's disease,  
CC diabetes, systemic lupus erythematosus or glomerulonephritis,  
CC neurodegenerative disorders including Parkinson's disease and Alzheimer's  
CC disease, wounds and hyperproliferative disorders including  
CC atherosclerosis or cancer, as well as bacterial, viral, fungal or  
CC parasitic infections. The polypeptide may also be used during gene  
CC therapy procedures and for identifying a binding partner by contacting  
CC the polypeptide with a binding partner and determining whether the  
CC binding partner increases or decreases the activity of the polypeptide.  
CC The current sequence is that of the human secreted protein of the  
CC invention.  
XX  
XX Sequence 112 AA;  
SQ  
Query Match 45.1%; Score 274.5; DB 7; Length 112;  
Best Local Similarity 96.4%; Pred. No. 1.2e-20;  
Matches 54; Conservative 1; Mismatches 0; Indels 1; Gaps 1;  
Oy 1 MARGSLRRLRLVGLWLLRLSVAGQAPGTPAPCSRGSWSADLCKMDCA-SC 55  
Db 1 MARGSLRRLRLVGLWLLRLSVAGQAPGTPAPCSRGSWSADLCKMDCTSC 56  
RESULT 6  
ADD38025  
ID ADD38025 standard; protein; 112 AA.  
XX  
XX ADD38025;  
AC  
XX  
XX 15-JAN-2004 (first entry)  
DT  
XX  
XX Human secreted protein #208.  
DE  
XX  
XX human secreted protein; Anti-allergic; Anti-inflammatory; Antibacterial;  
KW Anti-HIV; Cytostatic; Immunosuppressive; Hemostatic.  
KW  
XX

OS Homo sapiens.  
XX  
XX WO200290526-A2.  
FN  
XX  
XX 14-NOV-2002.  
PD  
XX  
XX 19-MAR-2002; 2002WO-US008279.  
PF  
XX  
XX 21-MAR-2001; 2001US-0277340P.  
PR  
XX 19-JUL-2001; 2001US-0306171P.  
PR  
XX 13-NOV-2001; 2001US-0331287P.  
PR  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
PA  
XX  
XX Rosen CA, Ruben SM;  
PI  
XX WPI; 2003-140218/13.  
DR  
XX  
XX New human secreted proteins and nucleic acid molecules, useful for  
PT preparing a diagnostic or pharmaceutical composition for diagnosing or  
PT treating allergic or asthmatic disorders, or related immediate  
PT hypersensitivity disorders.  
XX  
XX Claim 1; SEQ ID NO 507; 1323pp; English.  
PS  
XX  
XX The present invention relates to an isolated polypeptide or human  
CC secreted protein. The polypeptides, nucleic acid molecules, antibodies or  
CC their fragments, and agonists or antagonists that bind are useful for  
CC preparing a diagnostic or pharmaceutical composition for diagnosing or  
CC treating allergic or asthmatic disorders. The polypeptide is also useful  
CC for identifying a binding partner by contacting the polypeptide with a  
CC binding partner, and determining whether the binding partner increases or  
CC decreases the activity of the polypeptide. The polypeptides and nucleic  
CC acid molecules are also useful for detecting, preventing, diagnosing,  
CC prognosticating, treating or ameliorating inflammatory disorders,  
CC neoplastic diseases, wound healing and disorders of epithelial cell  
CC proliferation, immune disorders, cardiovascular disorders, blood-related  
CC disorders, infectious diseases, endocrine disorders, or gastrointestinal  
CC disorders. The nucleic acids are also useful for chromosome  
CC identification, radiation hybrid mapping or long-range restriction  
CC mapping, as molecular weight markers, or as hybridization or diagnostic  
CC probes. The polypeptides and antibodies are useful for providing  
CC immunological probes for differential identification of the tissues  
CC immunohistochemistry assays. The present sequence represents a human  
CC secreted protein.  
XX  
XX Sequence 112 AA;  
SQ  
Query Match 45.1%; Score 274.5; DB 7; Length 112;  
Best Local Similarity 96.4%; Pred. No. 1.2e-20;  
Matches 54; Conservative 1; Mismatches 0; Indels 1; Gaps 1;  
Oy 1 MARGSLRRLRLVGLWLLRLSVAGQAPGTPAPCSRGSWSADLCKMDCA-SC 55  
Db 1 MARGSLRRLRLVGLWLLRLSVAGQAPGTPAPCSRGSWSADLCKMDCTSC 56  
RESULT 7  
ADL71535  
ID ADL71535 standard; protein; 112 AA.  
XX  
XX ADL71535;  
AC  
XX  
XX 20-MAY-2004 (first entry)  
DT  
XX  
XX Novel human secreted protein seqid 139.  
DE  
XX  
XX antiinflammatory; neuroprotective; nootropic; antiparkinsonian;  
KW anticonvulsant; antilipemic; CNS; gynaecological; antiarthritic;  
KW antiasthmatic; anti-HIV; virucide; endocrine; cytostatic;  
KW immunosuppressive; anti-allergic; cardiovascular; respiratory;  
KW dermatological; antimicrobial; gastrointestinal; gene therapy;  
KW neurodegenerative disease; behavioral disorder; inflammatory condition;  
KW



KW hyperproliferative disorder; Alzheimer's disease; Parkinson's disease;  
KW Huntington's disease; metabolic disorder; Tay-Sach's disease;  
KW Leash-Nyhan syndrome; reproductive disorder; immunological disorder;  
KW arthritis; asthma; AIDS; endocrine disorder; immune disorder;  
KW Hodgkin's lymphoma; haematopoietic disorder; muscular disorder;  
KW leukaemia; autoimmune disorder; allergy; cancer; cardiovascular disorder;  
KW respiratory disorder; pulmonary disorder; connective tissue disorder;  
KW skin disorder; CNS disorder; congenital disorder; infectious disorder;  
KW gastrointestinal disorder; human; secreted protein.  
XX  
OS Homo sapiens.  
XX  
XX US2004034196-A1.  
XX  
XX 19-FEB-2004.  
XX  
XX 27-JAN-2003; 2003US-00351334.  
XX  
XX 30-JUL-1998; 98US-0094657P.  
PR 05-AUG-1998; 98US-0095486P.  
PR 06-AUG-1998; 98US-0095454P.  
PR 06-AUG-1998; 98US-0095455P.  
PR 12-AUG-1998; 98US-0096313P.  
PR 29-JUL-1999; 99WO-US017130.  
PR 24-JAN-2000; 2000US-00489847.  
PR 25-JAN-2002; 2002US-0350898P.  
XX  
XX (KOMA/) KOMATSULIS G A.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (DUAN/) DUAN D R.  
PA (MOOR/) MOORE P A.  
PA (SHI/) SHI Y.  
PA (LAF/) LAFLEUR D W.  
PA (WEI/) WEI Y.  
XX  
XX Komatsulis GA, Rosen CA, Ruben SM, Duan DR, Moore PA, Shi Y;  
PI Lafleur DW, Wei Y;  
PI  
XX  
XX WPI; 2004-180094/17.  
DR N-PSDB; ADL71419.  
XX  
XX New human secreted nucleic acid, useful for diagnosing and treating  
PT neurodegenerative, inflammatory, hyperproliferative, metabolic,  
PT reproductive, cardiovascular, respiratory or immunological disorders or  
PT diseases.  
XX  
XX Claim 11; SEQ ID NO 139; 234pp; English.  
PS  
XX  
XX The invention describes an isolated human nucleic acid molecule (I)  
CC comprising a polynucleotide having a nucleotide sequence at least 95%  
CC identical to: a sequence polynucleotide fragment of SEQ ID NO: X or of  
CC the cDNA sequence included in ATCC Deposit No: Z, which is hybridisable  
CC to SEQ ID NO: X; or a sequence encoding a polypeptide fragment, domain or  
CC epitope of SEQ ID NO: Y or a polypeptide sequence encoded by the cDNA  
CC sequence included in ATCC deposit No: Z, which is hybridisable to SEQ ID  
CC NO: X, having a biological activity. The nucleic acids and polypeptides,  
CC pharmaceutical formulations and kits are useful in diagnosing and  
CC treating neurodegenerative diseases states, behavioral disorders,  
CC inflammatory conditions, hyperproliferative disorders (e.g. Alzheimer's  
CC disease, Parkinson's disease or Huntington's disease), metabolic  
CC disorders (e.g. Tay-Sach's disease or Leash-Nyhan syndrome), reproductive  
CC disorders, immunological disorders (e.g. arthritis, asthma or AIDS),  
CC endocrine and immune disorders (e.g. Hodgkin's lymphoma), haematopoietic  
CC or muscular disorders (e.g. leukaemia), autoimmune disorders, allergy,  
CC cancer, cardiovascular, respiratory or pulmonary disorders, disorders or  
CC conditions afflicting connective tissue, skin disorders, CNS disorders,  
CC congenital disorders, infectious disorders and gastrointestinal  
CC disorders. This is the amino acid sequence of a novel human secreted  
CC protein of the invention. Note: This sequence does not appear in the US  
CC printed specification but is available in electronic format from the US  
CC patent office at ftp.segdata.uspto.gov/segdata.html?DocID=20040034196.  
XX

SQ Sequence 112 AA;  
Query Match 45.1%; Score 274.5; DB 8; Length 112;  
Best Local Similarity 96.4%; Pred. No. 1.2e-20;  
Matches 54; Conservative 1; Mismatches 0; Indels 1; Gaps 1;  
QY 1 MARGSLRRLRLVLGLMALLRSVAGQAPGTAPCSRGSWSADLDRKMDCA-SC 55  
Db 1 MARGSLRRLRLVLGLMALLRSVAGQAPGTAPCSRGSWSADLDRKMDCTSC 56  
RESULT 8  
ADA49370  
ID ADA49370 standard; peptide; 32 AA.  
XX  
XX ADA49370;  
XX  
XX 20-NOV-2003 (first entry)  
XX Human Fn14 cysteine rich domain.  
XX  
XX TALL-1; antagonist; immunosuppressive; antirheumatic; antiinflammatory;  
XX antiarthritic; dermatological; antidiabetic; neuroprotective;  
XX antithyroid; antipyretic; nephrotropic; vasotropic; vaccine;  
XX autoimmune disease; rheumatoid arthritis; systemic lupus erythematosus;  
XX insulin dependent diabetes mellitus; multiple sclerosis;  
XX myasthenia gravis; Grave's disease; autoimmune hemolytic anaemia;  
XX autoimmune thrombocytopenic purpura; Goodpasture's syndrome;  
XX pemphigus vulgaris; acute rheumatic fever;  
XX post-streptococcal glomerulonephritis; polyarteritis nodosa; Fn14; CRD;  
XX cysteine rich domain.  
XX  
XX Homo sapiens.  
XX WO2003035846-A2.  
XX  
XX 01-MAY-2003.  
XX  
XX 24-OCT-2002; 2002WO-US034376.  
XX  
XX 24-OCT-2001; 2001US-0345106P.  
PR 14-JAN-2002; 2002US-0348962P.  
PR 07-FEB-2002; 2002US-0354966P.  
PR 13-AUG-2002; 2002US-0403364P.  
XX  
XX (NAJE-) NAT JEWISH MEDICAL & RES CENT.  
XX  
XX Zhang G, Shu H, Liu Y, Xu L;  
XX  
XX WPI; 2003-403345/38.  
XX  
XX Novel TALL-1 antagonist protein useful for inhibiting TALL-1 biological  
PT activity in mammal, has a modification in the region connecting beta  
PT strands D and E that reduces the biological activity of TALL-1  
PT antagonist.  
XX  
XX Disclosure; Page 618; 618pp; English.  
XX  
XX The invention relates to a novel TALL-1 antagonist protein, comprising a  
CC sequence that differs from SEQ ID NO:2, or amino acids 134-285 of SEQ ID  
CC NO:2, by at least one modification in the region connecting <math>\beta</math>gtr; strands  
CC D and E that reduces the biological activity of the TALL-1 antagonist as  
CC compared to wild-type TALL-1. A protein of the invention has  
CC immunosuppressive, antirheumatic, antiinflammatory, antiarthritic,  
CC dermatological, antidiabetic, neuroprotective, antithyroid, antipyretic,  
CC nephrotropic, and vasotropic activity. A TALL-1 antagonist may be used in  
CC a vaccine. A protein of the invention is useful for inhibiting TALL-1  
CC biological activity in a mammal. TC is useful for treating autoimmune  
CC diseases, rheumatoid arthritis, systemic lupus erythematosus, insulin  
CC dependent diabetes mellitus, multiple sclerosis, myasthenia gravis,  
CC Grave's disease, autoimmune hemolytic anaemia, autoimmune  
CC thrombocytopenic purpura, Goodpasture's syndrome, pemphigus vulgaris,  
CC acute rheumatic fever, post-streptococcal glomerulonephritis and

```
CC polyarthritis nodosa. The present sequence represents a cysteine rich
CC domain (CRD) module of human Fn14.
XX
SQ Sequence 32 AA;
Query Match 31.4%; Score 191; DB 6; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.6e-12;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 36 CSRSSWSADLDKCMDCASCRRPHSDFLCIGC 67
DB 1 CSRSSWSADLDKCMDCASCRRPHSDFLCIGC 32
RESULT 9
AAU66196
ID AAU66196 standard; protein; 98 AA.
XX
AC AAU66196;
XX
XX 27-FEB-2002 (first entry)
XX
DE Propionibacterium acnes immunogenic protein #27092.
XX
XX SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
KW dermatological; osteopathic; neuroprotectant.
XX
XX Propionibacterium acnes.
XX
XX WO200181581-A2.
XX
XX 01-NOV-2001.
XX
XX 20-APR-2001; 2001WO-US012865.
XX
XX 21-APR-2000; 2000US-0199047P.
XX
XX 02-JUN-2000; 2000US-0208841P.
XX
XX 07-JUL-2000; 2000US-0216747P.
XX
XX (CORI-) CORIXA CORP.
XX
XX Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
XX L'maisonneuve J, Zhang Y, Jen S, Carter D;
XX
XX WPI; 2001-616774/71.
XX
XX N-PSDB; AAS59719.
XX
XX Propionibacterium acnes polypeptides and nucleic acids useful for
XX vaccinating against and diagnosing infections, especially useful for
XX treating acne vulgaris.
XX
XX Example 1; SEQ ID NO 27391; 1069pp; English.
XX
XX Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
XX polypeptides. The proteins and their associated DNA sequences are used in
XX the treatment, prevention and diagnosis of medical conditions caused by
XX P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
XX pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
XX P. acnes is also involved in infections of bone, joints and the central
XX nervous system, however it is particularly involved in the inflammatory
XX lesions associated with acne vulgaris. A method for detecting the
XX presence or absence of P. acnes in a patient comprises contacting a
XX sample with a binding agent that binds to the proteins of the invention
XX and determining the amount of bound protein in the sample. The
XX polypeptides may be used as antigens in the production of antibodies
XX specific for P. acnes proteins. These antibodies can be used to
XX downregulate expression and activity of P. acnes polypeptides and
XX therefore treat P. acnes infections. The antibodies may also be used as
XX diagnostic agents for determining P. acnes presence, for example, by
XX enzyme linked immunosorbent assay (ELISA). Note: The sequence data for
XX this patent did not form part of the printed specification, but was
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CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 98 AA;
Query Match 12.1%; Score 73.5; DB 4; Length 98;
Best Local Similarity 30.3%; Pred. No. 8.7;
Matches 33; Conservative 9; Mismatches 34; Indels 33; Gaps 8;
QY 18 WLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRPHSDFLCIGCA-----AA 70
DB 2 WSSLVESV-----PRATIC--GEEMHSGGDVVF---RVRRPVSTGVPGCAPCWCRCWAR 51
QY 71 PP---APFRLLPFI-----LGALS-LTFVLGLSGFLVRRRCR 105
DB 52 QPLVCSFWDRFWPVRSFGRRSRLSMGTSGGTRAMGLPAP--SWRRCR 98
RESULT 10
ABM62715
ID ABM62715 standard; protein; 98 AA.
XX
AC ABM62715;
XX
XX 20-OCT-2003 (first entry)
XX
XX Propionibacterium acnes predicted ORF-encoded polypeptide #27391.
XX
XX Acne vulgaris; antiseborrheic; dermatological; antibacterial;
XX immunostimulant; immune response; vaccine.
XX
XX Propionibacterium acnes.
XX
XX WO2003033515-A1.
XX
XX 24-APR-2003.
XX
XX 11-OCT-2002; 2002WO-US032727.
XX
XX 15-OCT-2001; 2001US-00978825.
XX
XX (CORI-) CORIXA CORP.
XX
XX Mitcham JL, Skeiky YAW, Persing DH, Bhatia A, Maisonneuve JL;
XX Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;
XX Barth B, Vallieve-Douglas J;
XX
XX WPI; 2003-381789/36.
XX
XX N-PSDB; ACF64648.
XX
XX New Propionibacterium acnes polypeptides and polynucleotides encoding the
XX polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
XX or for stimulating an immune response specific for a P. acnes protein.
XX
XX Example 1; SEQ ID NO 27391; 1481pp; English.
XX
XX The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
XX encoding a Propionibacterium acnes protein. The invention also relates to
XX polypeptides encoded by the polynucleotides (ABM35624-ABM64536) and to
XX immunogenic fragments of P. acnes polypeptides. The invention
XX additionally encompasses expression vectors and host cells comprising a
XX polynucleotide of the invention; antibodies against polypeptides of the
XX invention; fusion proteins comprising a polypeptide of the invention; a
XX method for stimulating an immune response specific for a P. acnes
XX polypeptide and an isolated T cell population comprising P. acnes polypeptides,
XX polynucleotides, antibodies, fusion proteins, T cell populations, or
XX antigen-presenting cells that express the polypeptide; a method and kit
XX for detecting or determining the presence or absence of P. acnes in a
XX patient; and a method for inhibiting the development of P. acnes in a
XX patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
XX proteins, T cell populations or antigen-presenting cells that express the
XX polypeptides are useful for diagnosing, preventing or treating acne
```

CC vulgaris, or for stimulating an immune response specific for a P. acnes  
CC protein. The polynucleotides can also be used as probes or primers for  
CC nucleic acid hybridization. The vaccine composition is useful for the  
CC stimulation of an immune response against P. acnes, or for treating acne,  
CC and the kit is useful for performing a diagnostic assay. The present  
CC sequence represents a polypeptide predicted to be encoded by an ORF (open  
CC reading frame) contained within the P. acnes polynucleotides of the  
CC invention. Note: The sequence data for this patent did not form part of  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
XX Sequence 98 AA;

Query Match 12.1%; Score 73.5; DB 6; Length 98;  
Best Local Similarity 30.3%; Pred. No. 8.7;  
Matches 33; Conservative 9; Mismatches 34; Indels 33; Gaps 8;  
QY 18 WLALRSVAGQAPGTAPCRSGSSWSADLDKCMDCASCRARPHSDFCLGCA-----AA 70  
DB 2 WSSLVESV-----PRATIC--GEWHSGGDVVF---RVRARPVSTGVGCPAPWCRCWSAR 51  
QY 71 PP---APRLLWPI-----LGGALS-LTFVLGLSGFLVWRCR 105  
DB 52 QPLVCSPWDRFPVWPSRRRLSMGGTSGGTRAWGLPAP--SWRRCR 98

RESULT 11  
ID AAE22260 standard; protein; 70 AA.  
XX  
XX AAE22260;  
XX  
XX 25-JUL-2002 (first entry)  
XX Human BAPF-R:Fc clone fusion protein, JST678.  
XX Human; BAPF receptor; BAPF-R; cytostatic; hypotensive; inflammation; TNF;  
XX Tumour Necrosis Factor; autoimmune disease; immunosuppressive; cancer;  
XX myasthenia gravis; hypertension; organ transplantation; drug screening;  
XX HIV; human immunodeficiency virus; genetic disorder; cardiovascular;  
XX renal; rheumatoid arthritis; systemic lupus erythematosus; amyloidosis;  
XX haemolytic anaemia; Chagas' disease; Grave's disease; glomerulonephritis;  
XX multiple myeloma; chromosomal mapping; tissue typing; drug screening;  
XX IGG; immunoglobulin G; fusion protein.  
XX  
XX Homo sapiens.  
XX  
XX WO200224909-A2.  
XX  
XX 28-MAR-2002.  
XX  
XX 06-SEP-2001; 2001WO-US028006.  
XX  
XX 18-SEP-2000; 2000US-0233152P.  
XX 21-SEP-2000; 2000US-0234140P.  
XX 13-FEB-2001; 2001US-0268499P.  
XX 14-AUG-2001; 2001US-0312185P.  
XX  
XX (BIOJ ) BIOGEN INC.  
XX  
XX Ambrose CM, Thompson JS;  
XX  
XX WPI; 2002-362428/39.  
XX  
XX New human BAPF receptor proteins and nucleic acids, useful for treating,  
XX preventing or delaying e.g. autoimmune diseases, cancers, inherited  
XX genetic disorders involving B-cells, cardiovascular disorders, or renal  
XX disorders.  
XX  
XX Claim 44; Fig 20; 164pp; English.  
XX  
XX The invention relates to human BAPF receptor (BAPF-R) nucleic acids and  
XX proteins. BAPF-R is a B-cell activating factor belonging to the Tumour  
CC

CC Necrosis Factor (TNF) family, which is associated with the expression of  
CC B-cells and immunoglobulins. The BAPF-R proteins, DNA and antibodies are  
CC useful for treating, preventing or delaying autoimmune diseases, cancer,  
CC tumorigenic conditions or inherited genetic disorders involving B-cells,  
CC hyperension, cardiovascular disorders, immunosuppressive diseases, renal  
CC disorders, inflammation, organ transplantation and HIV. Autoimmune  
CC diseases, which can be treated or prevented by BAPF-R, include systemic  
CC lupus erythematosus, rheumatoid arthritis, myasthenia gravis, autoimmune  
CC haemolytic anaemia, idiopathic thrombocytopenia purpura, Chagas' disease,  
CC Grave's disease, anti-phospholipid syndrome, Wegener's granulomatosis,  
CC poly-arthritis nodosa and rapidly progressive glomerulonephritis. Plasma  
CC cells disorders e.g., multiple myeloma, Waldenstrom's macroglobulinaemia,  
CC heavy-chain disease, primary or immunocyte-associated amyloidosis, and  
CC monoclonal gammopathy of undetermined significance. The nucleic acids,  
CC protein, protein homologues, and antibodies may further be used in  
CC screening assays, in detection assays (chromosomal mapping, tissue typing  
CC or forensic biology), predictive medicine (e.g. diagnostic or prognostic  
CC assays, monitoring clinical trials, or pharmacogenomic). The polypeptides  
CC are further useful as immunogens to raise anti-BPFR antibodies, or in  
CC screening drugs or compounds that modulate BAPF-R activity or expression.  
CC The present protein sequence is human BAPF-R:immunoglobulin G Fc region  
CC clone fusion protein  
XX  
XX Sequence 70 AA;

Query Match 11.5%; Score 70; DB 5; Length 70;  
Best Local Similarity 32.2%; Pred. No. 14;  
Matches 19; Conservative 6; Mismatches 28; Indels 6; Gaps 2;

QY 23 RSVAGEQAPGTAPCRSGSSWSADLDKCMDCASCRARPHSDFCLGCAAPAPRFLWLP 80  
DB 5 RSLGRDAPAPTPCNPACFCFDALVRHCVCGLLRPKP-----AGASSAPARTALQP 58

RESULT 12  
ID ABP06392 standard; protein; 79 AA.  
XX  
XX ABP06392;

XX 25-JUN-2002 (first entry)

XX Human ORFX protein sequence SEQ ID NO:12766.

XX Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;  
XX hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;  
XX degenerative disorder; osteoarthritis; neurodegenerative disorder;  
XX cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;  
XX hypertension; hypothyroidism; cholesterol ester storage disease;  
XX immune deficiency; immune disorder; infectious disease;  
XX autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;  
XX myasthenia gravis.  
XX  
XX Homo sapiens.  
XX  
XX WO200192523-A2.  
XX  
XX 06-DEC-2001.  
XX  
XX 29-MAY-2001; 2001WO-US010836.  
XX  
XX 30-MAY-2000; 2000US-0206132P.  
XX 29-AUG-2000; 2000US-0228716P.  
XX  
XX (CURA-) CURAGEN CORP.  
XX  
XX Shimkets RA, Leach MD;  
XX  
XX WPI; 2002-106308/14.  
XX N-PSDB; ABN22144.  
XX  
XX Novel human polypeptides and polynucleotides useful for diagnosing,  
XX preventing and treating cardiovascular disease, neurodegenerative,  
XX





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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 14, 2005, 07:10:21 ; Search time 127 Seconds  
(without alignments)  
293.302 Million cell updates/sec

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Perfect score: 608  
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Gapop 10.0 , Gapext 0.5

Searched: 1376875 seqs, 326749119 residues

Total number of hits satisfying chosen parameters: 626400

Minimum DB seq length: 0  
Maximum DB seq length: 114

Post-processing: Minimum Match 0%  
Maximum Match 100%  
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19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	608	100.0	114	15	US-10-062-599-59
3	274.5	45.1	112	15	US-10-351-334-139
4	74.5	12.3	112	16	US-10-437-963-108148
5	70	11.5	70	15	US-10-380-703-27
6	69.5	11.4	109	15	US-10-425-114-61480
7	68	11.2	70	15	US-10-380-703-21
8	68	11.2	70	15	US-10-380-703-30
9	67.5	11.1	72	16	US-10-437-963-163452
10	67	11.0	70	15	US-10-380-703-26
11	67	11.0	74	10	US-09-468-147-190
12	67	11.0	74	15	US-10-319-745-190
13	66	10.9	70	15	US-10-380-703-19

Sequence 28, Appl  
Sequence 22, Appl  
Sequence 24, Appl  
Sequence 31, Appl  
Sequence 32, Appl  
Sequence 28395, A  
Sequence 31337, A  
Sequence 210769,  
Sequence 153296,  
Sequence 20, Appl  
Sequence 23, Appl  
Sequence 29, Appl  
Sequence 53, Appl  
Sequence 175619,  
Sequence 189725,  
Sequence 169263, A  
Sequence 13, Appl  
Sequence 25, Appl  
Sequence 152927,  
Sequence 217717,  
Sequence 50873, A  
Sequence 179616,  
Sequence 181164,  
Sequence 8362, Ap  
Sequence 43778, A  
Sequence 215, App  
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Sequence 215, App  
Sequence 215, App  
Sequence 334, App  
Sequence 334, App

## ALIGNMENTS

## RESULT 1

US-10-062-831-59  
; Sequence 59, Application US/10062831  
; Publication No. US20030105297A1  
; GENERAL INFORMATION:  
; APPLICANT: Steven M. Ruben, et al.  
; TITLE OF INVENTION: 32 Human Secreted Proteins  
; FILE REFERENCE: PZ006P1  
; CURRENT APPLICATION NUMBER: US/10/062,831  
; CURRENT FILING DATE: 2002-02-05  
; PRIOR APPLICATION NUMBER: 09/690,454  
; PRIOR FILING DATE: 1998-11-10  
; PRIOR APPLICATION NUMBER: PCT/US98/10868  
; PRIOR FILING DATE: May 28, 1998  
; PRIOR APPLICATION NUMBER: 60/044,039  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/048,093  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/048,190  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/050,935  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/048,101  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/048,356  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/056,250  
; PRIOR FILING DATE: August 29, 1997  
; PRIOR APPLICATION NUMBER: 60/056,296  
; PRIOR FILING DATE: August 29, 1997  
; PRIOR APPLICATION NUMBER: 60/056,293  
; PRIOR FILING DATE: August 29, 1997  
; NUMBER OF SEQ ID NOS: 229  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 59  
; LENGTH: 114

;  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (114)  
; OTHER INFORMATION: Xaa equals stop translation  
US-10-062-831-59

Query Match 100.0%; Score 608; DB 14; Length 114;  
Best Local Similarity 100.0%; Pred. No. 4.6e-50;  
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRPH 60

Qy 61 SDFCLGCAAAAPPAPFRLWPILGGALSLTFVLGSLGFLVWRCRRRSSPPPX 114

Db 61 SDFCLGCAAAAPPAPFRLWPILGGALSLTFVLGSLGFLVWRCRRRSSPPPX 114

## RESULT 2

US-10-062-599-59  
; Sequence 59, Application US/10062599  
; Publication No. US20030195346A1  
; GENERAL INFORMATION:  
; APPLICANT: Steven M. Ruben, et al.  
; TITLE OF INVENTION: 32 Human Secreted Proteins

; FILE REFERENCE: PZ006P1

; CURRENT APPLICATION NUMBER: US/10/062,599

; CURRENT FILING DATE: 2002-02-05

; PRIOR APPLICATION NUMBER: 09/690,454

; PRIOR FILING DATE: 2000-10-18

; PRIOR APPLICATION NUMBER: 09/189,144

; PRIOR FILING DATE: 1998-11-10

; PRIOR APPLICATION NUMBER: 60/044,039

; PRIOR FILING DATE: May 30, 1997

; PRIOR APPLICATION NUMBER: 60/048,093

; PRIOR FILING DATE: May 30, 1997

; PRIOR APPLICATION NUMBER: 60/048,190

; PRIOR FILING DATE: May 30, 1997

; PRIOR APPLICATION NUMBER: 60/050,935

; PRIOR FILING DATE: May 30, 1997

; PRIOR APPLICATION NUMBER: 60/048,101

; PRIOR FILING DATE: May 30, 1997

; PRIOR APPLICATION NUMBER: 60/048,356

; PRIOR FILING DATE: May 30, 1997

; PRIOR APPLICATION NUMBER: 60/056,250

; PRIOR FILING DATE: August 29, 1997

; PRIOR APPLICATION NUMBER: 60/056,296

; PRIOR FILING DATE: August 29, 1997

; PRIOR APPLICATION NUMBER: 60/056,293

; PRIOR FILING DATE: August 29, 1997

; NUMBER OF SEQ ID NOS: 229

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 59

; LENGTH: 114

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: SITE

; LOCATION: (114)

; OTHER INFORMATION: Xaa equals stop translation

US-10-062-599-59

Query Match 100.0%; Score 608; DB 14; Length 114;

Best Local Similarity 100.0%; Pred. No. 4.6e-50;

Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRPH 60

Db 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASCRRPH 60

Qy 61 SDFCLGCAAAAPPAPFRLWPILGGALSLTFVLGSLGFLVWRCRRRSSPPPX 114  
Db 61 SDFCLGCAAAAPPAPFRLWPILGGALSLTFVLGSLGFLVWRCRRRSSPPPX 114

## RESULT 3

US-10-351-334-139  
; Sequence 139, Application US/10351334  
; Publication No. US20040034196A1  
; GENERAL INFORMATION:  
; APPLICANT: Komatsoulis et al.  
; TITLE OF INVENTION: 98 Human Secreted Proteins

; FILE REFERENCE: PZ031P2

; CURRENT APPLICATION NUMBER: US/10/351,334

; CURRENT FILING DATE: 2003-01-27

; PRIOR APPLICATION NUMBER: 60/350,898

; PRIOR FILING DATE: 2002-01-25

; PRIOR APPLICATION NUMBER: 09/489,847

; PRIOR FILING DATE: 2000-01-24

; PRIOR APPLICATION NUMBER: PCT/US99/17130

; PRIOR FILING DATE: 1999-07-29

; PRIOR APPLICATION NUMBER: 60/094,657

; PRIOR FILING DATE: 1998-07-30

; PRIOR APPLICATION NUMBER: 60/095,486

; PRIOR FILING DATE: 1998-08-05

; PRIOR APPLICATION NUMBER: 60/096,319

; PRIOR FILING DATE: 1998-08-12

; PRIOR APPLICATION NUMBER: 60/095,454

; PRIOR FILING DATE: 1998-08-06

; PRIOR APPLICATION NUMBER: 60/095,455

; PRIOR FILING DATE: 1998-08-06

; NUMBER OF SEQ ID NOS: 376

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 139

; LENGTH: 112

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-351-334-139

Query Match 45.1%; Score 274.5; DB 15; Length 112;

Best Local Similarity 96.4%; Pred. No. 1.8e-16;

Matches 54; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASC 55

Db 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAPCSRGSWSADLDKCMDCASC 56

## RESULT 4

US-10-437-963-108148

; Sequence 108148, Application US/10437963

; Publication No. US20040123343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 108148

; LENGTH: 112

; TYPE: PRT

; ORGANISM: Oryza sativa

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_1242C.1.pep



US-10-437-963-108148

Query Match 12.3%; Score 74.5; DB 16; Length 112;  
Best Local Similarity 34.5%; Pred. No. 17;  
Matches 20; Conservative 8; Mismatches 17; Indels 13; Gaps 3;  
QY 59 PHSD--FCLGCAAPAPPRLLWPILGGALSLTFLVLLSGFLVWRCRRRSPPPX 114  
DB 3 PHSDSIFLIGAAHQPRP-----PVVSNALT-----KLEVMAPRRRKQKHCPFPQ 49

RESULT 5

US-10-380-703-27  
; Sequence 27, Application US/10380703  
; Publication No. US20040072188A1  
; GENERAL INFORMATION:  
; APPLICANT: Biogen, Inc.  
; APPLICANT: Thompson, Jeffrey S  
; APPLICANT: Ambrose, Christine M  
; TITLE OF INVENTION: Receptor Nucleic Acids and Polypeptides  
; FILE REFERENCE: BIOG-0086  
; CURRENT APPLICATION NUMBER: US/10/380,703  
; CURRENT FILING DATE: 2003-07-28  
; PRIOR APPLICATION NUMBER: 60/233,152  
; PRIOR FILING DATE: 2000-09-18  
; PRIOR APPLICATION NUMBER: 60/234,140  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: 60/268,499  
; PRIOR FILING DATE: 2001-02-13  
; PRIOR APPLICATION NUMBER: 60/312,185  
; PRIOR FILING DATE: 2001-08-14  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 27  
; LENGTH: 70  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; NAME/KEY: VARIANT  
; LOCATION: (22)..(22)  
; OTHER INFORMATION: substitution  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (29)..(29)  
; OTHER INFORMATION: substitution  
US-10-380-703-27

Query Match 11.5%; Score 70; DB 15; Length 70;  
Best Local Similarity 32.2%; Pred. No. 28;  
Matches 19; Conservative 6; Mismatches 28; Indels 6; Gaps 2;  
QY 23 RSVAGEQAGTAPCSRSGSSWSADLDKCMDCASCRA-RPHSDFCLGCAAPAPPRLLWP 80  
DB 5 RSLGRDAPPTPCNPABCFDALVRHVCAGLLTPRPKP-----AGASSPAPRTALQP 58

RESULT 6

US-10-425-114-61480  
; Sequence 61480, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaska, Jack E  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128

; SEQ ID NO 61480  
; LENGTH: 109  
; TYPE: PRT  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB148-012-G11\_FLI pep  
US-10-425-114-61480  
Query Match 11.4%; Score 69.5; DB 15; Length 109;  
Best Local Similarity 29.7%; Pred. No. 48;  
Matches 27; Conservative 9; Mismatches 36; Indels 19; Gaps 5;  
QY 5 SLRLRLRLVLGLMLALLRSVAGEQAGTAPCSRSGSSWSADLD---KCMDCASCRCARPHS 61  
DB 20 SMPLLIRYVLFLLT-----NNVAFCSVDDRMRLDYGVSIMARNCRALRSQSHT 66  
QY 62 DF-CLGC-AAAPPAPPRLLWP-PILGGALSLT 89  
DB 67 RIRCAACLSAADPQPHDLCSFYNGRALCMT 97

RESULT 7

US-10-380-703-21  
; Sequence 21, Application US/10380703  
; Publication No. US20040072188A1  
; GENERAL INFORMATION:  
; APPLICANT: Biogen, Inc.  
; APPLICANT: Thompson, Jeffrey S  
; APPLICANT: Ambrose, Christine M  
; TITLE OF INVENTION: Receptor Nucleic Acids and Polypeptides  
; FILE REFERENCE: BIOG-0086  
; CURRENT APPLICATION NUMBER: US/10/380,703  
; CURRENT FILING DATE: 2003-07-28  
; PRIOR APPLICATION NUMBER: 60/233,152  
; PRIOR FILING DATE: 2000-09-18  
; PRIOR APPLICATION NUMBER: 60/234,140  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: 60/268,499  
; PRIOR FILING DATE: 2001-02-13  
; PRIOR APPLICATION NUMBER: 60/312,185  
; PRIOR FILING DATE: 2001-08-14  
; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 21  
; LENGTH: 70  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; NAME/KEY: VARIANT  
; LOCATION: (22)..(22)  
; OTHER INFORMATION: substitution  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (23)..(23)  
; OTHER INFORMATION: substitution  
; FEATURE:  
; NAME/KEY: VARIANT  
; LOCATION: (29)..(29)  
; OTHER INFORMATION: substitution  
US-10-380-703-21

Query Match 11.2%; Score 68; DB 15; Length 70;  
Best Local Similarity 30.5%; Pred. No. 44;  
Matches 18; Conservative 7; Mismatches 28; Indels 6; Gaps 2;  
QY 23 RSVAGEQAGTAPCSRSGSSWSADLDKCMDCASCRA-RPHSDFCLGCAAPAPPRLLWP 80  
DB 5 RSLGRDAPPTPCNQAECFDPVLRHVCAGLLTPRPKP-----AGASSPAPRTALQP 58  
RESULT 8  
US-10-380-703-30  
; Sequence 30, Application US/10380703

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Query Match      11.0%; Score 67; DB 15; Length 70;
Best Local Similarity 30.5%; Pred. No. 54;
Matches 18; Conservative 7; Mismatches 28; Indels 6; Gaps
Qy 23 RSVAGQAGTGTATPCSRGSSWSADLDDKMDASCRA-RPHSDFCLGCAAPPAFFLLWP 80
      ||| ||| ||| : : : ||| ||| : ||| |||
Db 5 RSLRGDAPATPCNPABECFSLVHRHCVAGLLTFRPKP-----AGASSPAPRTALQP 58

RESULT 11
US-09-468-147-190
; Sequence 190, Application US/09468147A
; Publication No. US20030049601A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Schlauder, George G.
; APPLICANT: Erker, James C.
; APPLICANT: Desai, Suresh M.
; APPLICANT: Dawson, George J.
; APPLICANT: Mushahwar, I. K.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; TITLE OF INVENTION: HEPATITIS E VIRUS
; FILE REFERENCE: 6232.US.P1
; CURRENT APPLICATION NUMBER: US/09/468,147A
; CURRENT FILING DATE: 1999-12-21
; EARLIER APPLICATION NUMBER: US 09/173,141
; EARLIER FILING DATE: 1998-10-15
; EARLIER APPLICATION NUMBER: US 60/061,199

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; EARLIER FILING DATE: 1997-10-15
; NUMBER OF SEQ ID NOS: 258
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 190
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Hepatitis E Virus
; FEATURE:
; OTHER INFORMATION: z12-orf3.pep
US-09-468-147-190

Query Match      11.0%; Score 67; DB 10; Length 74;
Best Local Similarity 28.2%; Pred. No. 57;
Matches 24; Conservative 14; Mismatches 21; Indels 26; Gaps 5;

Qy 30 APGTAPCSGSSWSADLDKCMDCASCRAHPHSDFCGLGCAAAPPPFRLWLPILGGALSLT 89
Db 8 SPMGSPCALG-----LFCC--CSSC-----FCLCCPRHPA--SRLAAVVGAAAVP 50

Qy 90 FVLGSLGFLVWRCRRERSPPPX 114
Db 51 AVVSGVTGLIL-----SPSPS 66

RESULT 12
US-10-319-745-190
; Sequence 190, Application US/10319745
; Publication No. US20030211467A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Schlauder, George G.
; APPLICANT: Erker, James C.
; APPLICANT: Desai, Suresh M.
; APPLICANT: Dawson, George J.
; APPLICANT: Mushahwar, I. K.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; FILE REFERENCE: 6232.US.P1
; CURRENT APPLICATION NUMBER: US/10/319,745
; CURRENT FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: US/09/468,147A
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1998-10-15
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-15
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-15
; NUMBER OF SEQ ID NOS: 258
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 190
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Hepatitis E Virus
; FEATURE:
; OTHER INFORMATION: z12-orf3.pep
US-10-319-745-190

Query Match      11.0%; Score 67; DB 15; Length 74;
Best Local Similarity 28.2%; Pred. No. 57;
Matches 24; Conservative 14; Mismatches 21; Indels 26; Gaps 5;

Qy 30 APGTAPCSGSSWSADLDKCMDCASCRAHPHSDFCGLGCAAAPPPFRLWLPILGGALSLT 89
Db 8 SPMGSPCALG-----LFCC--CSSC-----FCLCCPRHPA--SRLAAVVGAAAVP 50

Qy 90 FVLGSLGFLVWRCRRERSPPPX 114
Db 51 AVVSGVTGLIL-----SPSPS 66

RESULT 13
US-10-380-703-19
; Sequence 19, Application US/10380703
; Publication No. US20040072188A1
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; GENERAL INFORMATION:
; APPLICANT: Biogen, Inc.
; APPLICANT: Thompson, Jeffrey S
; APPLICANT: Ambrose, Christine M
; TITLE OF INVENTION: Receptor Nucleic Acids and Polypeptides
; FILE REFERENCE: BIOG-0086
; CURRENT APPLICATION NUMBER: US/10/380,703
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: 60/233,152
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: 60/234,140
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/268,499
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/312,185
; PRIOR FILING DATE: 2001-08-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (22)..(22)
; OTHER INFORMATION: substitution
; NAME/KEY: VARIANT
; LOCATION: (23)..(23)
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; LOCATION: (24)..(24)
; OTHER INFORMATION: substitution
; NAME/KEY: VARIANT
; LOCATION: (29)..(29)
; OTHER INFORMATION: substitution
US-10-380-703-19

Query Match      10.9%; Score 66; DB 15; Length 70;
Best Local Similarity 30.5%; Pred. No. 67;
Matches 18; Conservative 7; Mismatches 28; Indels 6; Gaps 2;

Qy 23 RSVAGEAPGTAPCSGSSWSADLDKCMDCASCRA--RPHSDFCLGCAAAPPPFLLWP 80
Db 5 RSLGRDAPAPTPCQTECFDPLVRHCVACGLLTTPRKP-----AGASSPAPRTALQP 58

RESULT 14
US-10-380-703-28
; Sequence 28, Application US/10380703
; Publication No. US20040072188A1
; GENERAL INFORMATION:
; APPLICANT: Biogen, Inc.
; APPLICANT: Thompson, Jeffrey S
; APPLICANT: Ambrose, Christine M
; TITLE OF INVENTION: Receptor Nucleic Acids and Polypeptides
; FILE REFERENCE: BIOG-0086
; CURRENT APPLICATION NUMBER: US/10/380,703
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: 60/233,152
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: 60/234,140
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/268,499
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/312,185
; PRIOR FILING DATE: 2001-08-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 70
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; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (22)..(22)
; OTHER INFORMATION: substitution
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (23)..(23)
; OTHER INFORMATION: substitution
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (24)..(24)
; OTHER INFORMATION: substitution
; OTHER INFORMATION: substitution
US-10-380-703-28

Query Match      10.9%; Score 66; DB 15; Length 70;
Best Local Similarity 30.5%; Pred. No. 67;
Matches 18; Conservative 7; Mismatches 28; Indels 6; Gaps 2;

QY      23 RSVAGEQAPGTAPCSRSSWSADLDKCMDASCRA-RPHSDFCLGCAAPAPFRLMLP 80
Db      5 RSLGRDAPAPTPCNPQTECFDLVHRHCVACGLLTPRPKP-----AGASSPAPRTALQP 58

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RESULT 15
US-10-380-703-22
; Sequence 22, Application US/10380703
; Publication No. US20040072188A1
; GENERAL INFORMATION:
; APPLICANT: Biogen, Inc.
; APPLICANT: Thompson, Jeffrey S
; APPLICANT: Ambrose, Christine M
; TITLE OF INVENTION: Receptor Nucleic Acids and Polypeptides
; FILE REFERENCE: BIOG-0086
; CURRENT APPLICATION NUMBER: US/10/380,703
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: 60/233,152
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: 60/234,140
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/268,499
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/312,185
; PRIOR FILING DATE: 2001-08-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (22)..(22)
; OTHER INFORMATION: substitution
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (29)..(29)
; OTHER INFORMATION: substitution
US-10-380-703-22

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Query Match      10.7%; Score 65; DB 15; Length 70;
Best Local Similarity 30.5%; Pred. No. 84;
Matches 18; Conservative 6; Mismatches 29; Indels 6; Gaps 2;

QY      23 RSVAGEQAPGTAPCSRSSWSADLDKCMDASCRA-RPHSDFCLGCAAPAPFRLMLP 80
Db      5 RSLGRDAPAPTPCNPQTECFDLVHRHCVACGLLTPRPKP-----AGASSPAPRTALQP 58

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Search completed: February 14, 2005, 07:17:26  
Job time : 127 secs

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OM protein - protein search, using sw model

Run on: February 14, 2005, 06:59:26 ; Search time 42 Seconds  
(without alignments)  
202.619 Million cell updates/sec

Title: US-10-062-831-59  
Perfect score: 608  
Sequence: 1 MARGSLRRLRLVGLWLA.....LSGFLVWRCRRSSPPPX 114

Scoring table: BLOSUM62DX  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 338531

Minimum DB seq length: 0  
Maximum DB seq length: 114

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	608	100.0	114	4	US-09-690-454-59
2	274.5	45.1	112	4	US-09-489-847-139
3	68	11.2	112	4	US-09-252-991A-21707
4	64	10.5	95	4	US-09-252-991A-16640
5	63	10.4	73	4	US-09-270-767-36705
6	63	10.4	73	4	US-09-270-767-51922
7	61.5	10.1	79	4	US-09-513-999C-4659
8	61.5	10.1	80	4	US-09-471-276-813
9	61.5	10.1	95	4	US-09-621-976-5253
10	61	10.0	71	4	US-09-107-532A-4242
11	60.5	10.0	75	6	5189019-4
12	60.5	10.0	75	6	5189019-4
13	60.5	10.0	94	3	US-08-851-843A-215
14	60.5	10.0	94	3	US-08-974-549A-334
15	60.5	10.0	94	3	US-08-854-050-215
16	60.5	10.0	94	3	US-09-430-323-215
17	60.5	10.0	94	4	US-09-402-181B-334
18	60.5	10.0	94	4	US-09-721-456-334
19	60.5	10.0	108	4	US-09-270-767-35067
20	60.5	10.0	108	4	US-09-270-767-50284
21	60	9.9	93	4	US-09-270-767-50284
22	60	9.9	93	4	US-09-270-767-50536
23	60	9.9	109	4	US-09-252-991A-29444
24	59.5	9.8	71	4	US-09-252-991A-26803
25	59.5	9.8	99	4	US-09-252-991A-25315
26	59.5	9.8	103	4	US-09-489-039A-7227
27	59	9.7	68	1	US-07-696-051B-1

28	59	9.7	68	1	US-07-924-063A-1	Sequence 1, Appli
29	59	9.7	68	1	US-08-138-340B-2	Sequence 2, Appli
30	58.5	9.6	69	4	US-09-205-258-439	Sequence 439, App
31	58	9.5	98	4	US-09-252-991A-31510	Sequence 31510, A
32	58	9.5	111	4	US-09-252-991A-17821	Sequence 17821, A
33	57.5	9.5	82	4	US-09-107-433-3031	Sequence 3031, Ap
34	57.5	9.5	96	4	US-09-252-991A-23413	Sequence 23413, A
35	57.5	9.5	104	4	US-09-252-991A-23645	Sequence 23645, A
36	57.5	9.5	110	4	US-09-252-991A-18800	Sequence 18800, A
37	57	9.4	48	4	US-09-471-276-1121	Sequence 1121, Ap
38	57	9.4	102	4	US-09-252-991A-22067	Sequence 22067, A
39	56.5	9.3	100	4	US-09-127-578-6	Sequence 6, Appli
40	56.5	9.3	111	4	US-09-252-991A-23578	Sequence 23578, A
41	56	9.2	85	1	US-08-468-347-18	Sequence 18, Appl
42	56	9.2	85	2	US-08-467-389-18	Sequence 18, Appl
43	56	9.2	85	2	US-08-779-379-18	Sequence 18, Appl
44	56	9.2	85	2	US-08-469-219-18	Sequence 18, Appl
45	56	9.2	85	3	US-09-228-152-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1  
US-09-690-454-59  
; Sequence 59, Application US/09690454  
; Patent No. 6531447  
; GENERAL INFORMATION:  
; APPLICANT: Steven M. Ruben, et al.  
; TITLE OF INVENTION: 32 Human Secreted Proteins  
; FILE REFERENCE: P2006P1  
; CURRENT APPLICATION NUMBER: US/09/690,454  
; CURRENT FILING DATE: 2000-10-18  
; PRIOR APPLICATION NUMBER: 09/189,144  
; PRIOR FILING DATE: 1998-11-10  
; PRIOR APPLICATION NUMBER: 60/044,039  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/048,093  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/048,190  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/050,935  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/048,101  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/048,356  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/056,250  
; PRIOR FILING DATE: August 29, 1997  
; PRIOR APPLICATION NUMBER: 60/056,296  
; PRIOR FILING DATE: August 29, 1997  
; PRIOR APPLICATION NUMBER: 60/056,293  
; PRIOR FILING DATE: August 29, 1997  
; NUMBER OF SEQ ID NOS: 229  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 59  
; LENGTH: 114  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (114)  
; OTHER INFORMATION: Xaa equals stop translation  
US-09-690-454-59

Query Match 100.0%; Score 608; DB 4; Length 114;  
Best Local Similarity 100.0%; Pred.No. 6e-58;  
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MARGSLRRLRLVGLWLAIRSRVAGEQAPCTAPCSGSSWSADLDKCMDCASCARAPH 60  
DB 1 MARGSLRRLRLVGLWLAIRSRVAGEQAPCTAPCSGSSWSADLDKCMDCASCARAPH 60

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QY      61  SDFCLGCAAAAPPAPFRLLPILGALLSLTFVLGSLGFLWRRCRERSPPPX 114
      |||
      |||
Db      61  SDFCLGCAAAAPPAPFRLLPILGALLSLTFVLGSLGFLWRRCRERSPPPX 114
      |||
      |||

RESULT 2
US-09-489-847-139
; Sequence 139, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: P2031P1
; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454
; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 139
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-489-847-139

Query Match      45.1%; Score 274.5; DB 4; Length 112;
Best Local Similarity 96.4%; Pred. No. 4e-22;
Matches 54; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY      1  MARGSLRRLLRLVLGLWALLRSVAGEAGPTAPCSRGSSWSADLDKMDCA-SC 55
      |||
      |||
Db      1  MARGSLRRLLRLVLGLWALLRSVAGEAGPTAPCSRGSSWSADLDKMDCA-SC 56
      |||
      |||

RESULT 3
US-09-252-991A-21707
; Sequence 21707, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21707
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21707

Query Match      11.2%; Score 68; DB 4; Length 112;
Best Local Similarity 26.8%; Pred. No. 6.2;
Matches 34; Conservative 11; Mismatches 26; Indels 56; Gaps 9;

QY      23  RSVAGEQA---PGTAP-----CSRGSSWSADLDKMDCAACRAPHDFCLGCA 68
      |||
      |||
Db      6  RSPRGRSRPPPGSPATVRGPGVGCAR-SPW-----ASVRSRGT---GCG 50
      |||
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US-09-270-767-51922  
; Sequence 51922, Application US/09270767  
; Patent No. 6703491

; GENERAL INFORMATION:

; APPLICANT: Homburger et al.

; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

; FILE REFERENCE: File Reference: 7326-094

; CURRENT APPLICATION NUMBER: US/09/270,767

; CURRENT FILING DATE: 1999-03-17

; NUMBER OF SEQ ID NOS: 62517

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 51922

; LENGTH: 73

; TYPE: PRT

; ORGANISM: Drosophila melanogaster

US-09-270-767-51922

Query Match

10.4%; Score 63; DB 4; Length 73;

Best Local Similarity 22.0%; Pred. No. 13;

Matches 20; Conservative 7; Mismatches 20; Indels 44; Gaps 3;

QY 24 SVAGEOAPCTAPCSRGSWSADLCKMDCASCRCRPHSDFCIGCAAPAPRLWPILG 83

Db 27 AVAGDRGTGVNARDW---LHQC-----AFAPHPPEP----- 58

QY 84 GALSITFVLGLSGFLVWRRCRRSSPPX 114

Db 59 -----RWENCHLEPAALPPG 73

RESULT 7

US-09-513-999C-4659

; Sequence 4659, Application US/09513999C

; Patent No. 6783961

; GENERAL INFORMATION:

; APPLICANT: Dumas Milne Edwards, J.B.

; APPLICANT: Duclert, A.

; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

; Patent No. 6783961

; FILE REFERENCE: 59.US2.REG

; CURRENT APPLICATION NUMBER: US/09/513,999C

; CURRENT FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: US 60/122,487

; PRIOR FILING DATE: 1999-02-26

; NUMBER OF SEQ ID NOS: 36681

; SOFTWARE: Patent.pm

; SEQ ID NO 4659

; LENGTH: 79

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: SIGNAL

; LOCATION: -16...-1

; OTHER INFORMATION: score 14.8

; OTHER INFORMATION: seq SLPLLLLLGAWA/IP

US-09-513-999C-4659

Query Match

10.1%; Score 61.5; DB 4; Length 79;

Best Local Similarity 29.5%; Pred. No. 21;

Matches 23; Conservative 12; Mismatches 28; Indels 15; Gaps 4;

QY 10 LRLVLGLWALLRSVAGEOAPGTAPCSR---GSSWSADLCKMDCASCRCRPHSDFCIG 66

Db 7 LLLLLLGGW--AIPGGLDRAPLTATAPQDDDEMYSAHPAHLKDCACRAVAYO----- 59

QY 67 CAAPAPPAPF--RLLWPIL 82

Db 60 ---VSPSPSPALLTPLL 74

RESULT 8

US-09-471-276-813

; Sequence 813, Application US/09471276

; Patent No. 6822072

; GENERAL INFORMATION:

; APPLICANT: Dumas Milne Edwards, J.B.

; APPLICANT: Duclert A.

; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

; Patent No. 6822072

; FILE REFERENCE: GENSET.025CPI

; CURRENT APPLICATION NUMBER: US/09/471,276

; CURRENT FILING DATE: 1999-12-21

; EARLIER APPLICATION NUMBER: 09/057,719

; EARLIER FILING DATE: 1998-04-09

; EARLIER APPLICATION NUMBER: 09/069,047

; EARLIER FILING DATE: 1998-04-28

; EARLIER APPLICATION NUMBER: PCT/IB99/00712

; EARLIER FILING DATE: 1999-04-09

; NUMBER OF SEQ ID NOS: 1622

; SOFTWARE: Patent.pm

; SEQ ID NO 813

; LENGTH: 80

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: SIGNAL

; LOCATION: -16...-1

US-09-471-276-813

Query Match

10.1%; Score 61.5; DB 4; Length 80;

Best Local Similarity 29.5%; Pred. No. 21;

Matches 23; Conservative 12; Mismatches 28; Indels 15; Gaps 4;

QY 10 LRLVLGLWALLRSVAGEOAPGTAPCSR---GSSWSADLCKMDCASCRCRPHSDFCIG 66

Db 7 LLLLLLGGW--AIPGGLDRAPLTATAPQDDDEMYSAHPAHLKDCACRAVAYO----- 59

QY 67 CAAPAPPAPF--RLLWPIL 82

Db 60 ---VSPSPSPALLTPLL 74

RESULT 9

US-09-621-976-5253

; Sequence 5253, Application US/09621976

; Patent No. 6639063

; GENERAL INFORMATION:

; APPLICANT: Dumas Milne Edwards, J.B.

; APPLICANT: Jobert, S.

; TITLE OF INVENTION: ESTs and Encoded Human Proteins.

; FILE REFERENCE: GENSET.054PR2

; CURRENT APPLICATION NUMBER: US/09/621,976

; CURRENT FILING DATE: 2000-07-21

; NUMBER OF SEQ ID NOS: 19335

; SOFTWARE: Patent.pm

; SEQ ID NO 5253

; LENGTH: 95

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: SIGNAL

; LOCATION: -24...-1

US-09-621-976-5253

Query Match

10.1%; Score 61.5; DB 4; Length 95;

Best Local Similarity 23.9%; Pred. No. 26;

Matches 26; Conservative 9; Mismatches 31; Indels 43; Gaps 5;

QY 9 LRLVLGLWALLRSVAGEOAPGTAPCSRGSWSADLCKMDCASCRCRPHSDFCIGCA 68

Db 1 MARFLTCTWLLIG--PGLLATVRAECQ-----DCATC----- 33

QY 69 AAPAPPFLLWPILGGALSLTFLV-----GLLSGFLVWRRCRRSSP 111





;; FILING DATE: 06-MAY-1997  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/846,017  
;; FILING DATE: 25-APR-1997  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/844,419  
;; FILING DATE: 18-APR-1997  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/724,643  
;; FILING DATE: 01-OCT-1996  
;; CLASSIFICATION:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Apple, Randolph T.  
;; REGISTRATION NUMBER: 36,429  
;; REFERENCE/DOCKET NUMBER: 015389-002930US  
;; TELEPHONE: (415) 576-0200  
;; TELEFAX: (415) 576-0300  
;; INFORMATION FOR SEQ ID NO: 215:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 94 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS:  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
US-08-851-843A-215

Query Match 10.0%; Score 60.5; DB 3; Length 94;  
Best Local Similarity 34.0%; Pred. No. 32;  
Matches 17; Conservative 4; Mismatches 22; Indels 7; Gaps 2;

QY 36 CARGKWPFRPPPR-----CRALPAAEPCAPCCAATTARC-CRWPRSCGA 85  
DB 6 CARGKWPFRPPPR-----CRALPAAEPCAPCCAATTARC-CRWPRSCGA 48

RESULT 14  
US-08-974-549A-334  
; Sequence 334, Application US/08974549A  
; Patent No. 6166178  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; APPLICANT: Lingner, Joachim  
; APPLICANT: Nakamura, Toru  
; APPLICANT: Chapman, Karen B.  
; APPLICANT: Morin, Gregg B.  
; APPLICANT: Harley, Calvin H.  
; APPLICANT: Andrews, William H.  
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
; NUMBER OF SEQUENCES: 727  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/974,549A  
; FILING DATE: 19-NOV-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/724,643  
; FILING DATE: 01-OCT-1996  
; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 08/844,419  
;; FILING DATE: 18-APR-1997  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/846,017  
;; FILING DATE: 25-APR-1997  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/851,843  
;; FILING DATE: 06-MAY-1997  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/854,050  
;; FILING DATE: 09-MAY-1997  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/911,312  
;; FILING DATE: 14-AUG-1997  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/912,951  
;; FILING DATE: 14-AUG-1997  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/915,503  
;; FILING DATE: 14-AUG-1997  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: WO PCT/US97/17618  
;; FILING DATE: 01-OCT-1997  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: WO PCT/US97/17885  
;; FILING DATE: 01-OCT-1997  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Apple, Randolph Ted  
;; REGISTRATION NUMBER: 36,429  
;; REFERENCE/DOCKET NUMBER: 015389-002610US  
;; TELEPHONE: (415) 576-0200  
;; TELEFAX: (415) 576-0300  
;; INFORMATION FOR SEQ ID NO: 334:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 94 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS:  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
US-08-974-549A-334

Query Match 10.0%; Score 60.5; DB 3; Length 94;  
Best Local Similarity 34.0%; Pred. No. 32;  
Matches 17; Conservative 4; Mismatches 22; Indels 7; Gaps 2;

QY 36 CARGKWPFRPPPR-----CRALPAAEPCAPCCAATTARC-CRWPRSCGA 85  
DB 6 CARGKWPFRPPPR-----CRALPAAEPCAPCCAATTARC-CRWPRSCGA 48

RESULT 15  
US-08-854-050-215  
; Sequence 215, Application US/08854050  
; Patent No. 6261836  
; GENERAL INFORMATION:  
; APPLICANT: Cech, Thomas R.  
; APPLICANT: Lingner, Joachim  
; APPLICANT: Nakamura, Toru  
; APPLICANT: Chapman, Karen B.  
; APPLICANT: Morin, Gregg B.  
; APPLICANT: Harley, Calvin  
; APPLICANT: Andrews, William H.  
; TITLE OF INVENTION: No. 6261836el Telomerase  
; NUMBER OF SEQUENCES: 225  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 94111  
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 215:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 94 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-854-050-215

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Query Match      10.0%; Score 60.5; DB 3; Length 94;
Best Local Similarity 34.0%; Pred. NO. 32;
Matches 17; Conservative 4; Mismatches 22; Indels 7; Gaps 2;

Qy      36 CSRGSSWSADLDKCMDCASCRRPHSDFCLGCAAAPPPFLLWPIILGGA 85
Db      6 CARGKWPFRPPPR-----CRALPAAEPCAPCCATTARC-CRWPRSCGA 48

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Search completed: February 14, 2005, 07:14:45  
Job time : 43 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2005, 18:03:08 ; Search time 10.2851 Seconds  
(without alignments)  
327.424 Million cell updates/sec

Title: US-10-062-831-59\_COPY\_1\_35

Perfect score: 170

Sequence: 1 MARGSLRLRLVLLGLWLALLRSVAGEQAPGTAP 35

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	59	34.7	228	2 S53504	extensin-like prot
2	55	32.4	289	2 T34688	probable lipoprote
3	54	31.8	462	2 T17480	endo-xyranase homo
4	54	31.8	556	2 C87609	sensor histidine k
5	54	31.8	647	2 JE0337	Frizzled-1 protein
6	53	31.2	127	2 C85091	arabinogalactan-pr
7	53	31.2	461	2 S75711	hypothetical prote
8	52	30.6	499	2 T45923	hypothetical prote
9	52	30.6	538	2 F83622	probable pernease
10	52	30.6	957	2 A47531	glutaryl aminopept
11	51.5	30.3	537	2 T02982	probable sucrose t
12	51	30.0	245	2 AD0753	flagellar biosynth
13	51	30.0	245	2 S78698	probable export pr
14	51	30.0	313	2 F75251	cytochrome C oxida
15	51	30.0	520	2 S70198	glycosyltransferas
16	50.5	29.7	432	2 I48343	interleukin-11 rec
17	50.5	29.7	451	2 F87407	probable phosphodi
18	50.5	29.7	581	2 T44942	cytochrome-c oxida
19	50.5	29.7	625	2 B96710	hypothetical prote
20	50	29.4	133	2 C86473	arabinogalactan-pr
21	50	29.4	220	2 A75362	hypothetical prote
22	50	29.4	343	2 D75370	hypothetical prote
23	50	29.4	364	2 B72672	hypothetical prote
24	50	29.4	394	2 T04631	hypothetical prote
25	50	29.4	486	2 S71583	1-aminocyclopropan
26	50	29.4	626	2 H87648	cell division prot
27	49.5	29.1	379	2 D91078	probable lipoprote
28	49.5	29.1	379	2 E85923	lipoprotein (impor
29	49.5	29.1	379	2 B55522	lipoprotein D prec

30	49.5	29.1	478	2 JC4838	bone morphogenetic
31	49.5	29.1	809	2 AE0374	probable permease
32	49	28.8	222	2 AE1826	hypothetical prote
33	49	28.8	257	2 C70635	hypothetical prote
34	49	28.8	301	2 B84254	hypothetical prote
35	49	28.8	305	2 A12658	conserved hypothat
36	49	28.8	326	2 AC0705	vitamin B12 transp
37	49	28.8	347	2 G97440	hypothetical prote
38	49	28.8	355	2 AD2973	hypothetical prote
39	49	28.8	355	2 G98309	probable ABC trans
40	49	28.8	543	2 B54424	acrosomal protein
41	49	28.8	880	2 T02245	hypothetical prote
42	48.5	28.5	175	2 AE3293	hypothetical prote
43	48.5	28.5	262	2 S60213	fomC protein - Str
44	48.5	28.5	411	2 D83307	probable FMN oxido
45	48.5	28.5	484	2 T06063	hypothetical prote

## ALIGNMENTS

### RESULT 1

S53504

extensin-like protein S3 - alfalfa

C:Species: Medicago sativa (alfalfa)

C>Date: 15-Jul-1995 #sequence\_revision 03-Nov-1995 #text\_change 09-Jul-2004

C:Accession: S53504

R:Abraham, S.; Hayes, C.M.; Watson, J.M.

Plant Mol. Biol. 27, 513-528, 1995

A>Title: Expression patterns of three genes in the stem of lucerne (Medicago sativa).

A:Reference number: S53504; MUID:95201245; PMID:7894016

A:Accession: S53504

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-228 <ABR>

A:Cross-references: UNIPROT:Q43558; GB:L36120; NID:G535585; PIDN:AAB41815.1; PID:G535585

C:Superfamily: proline-rich protein 3

Query Match 34.7%; Score 59; DB 2; Length 228;

Best Local Similarity 50.0%; Pred. No. 1.8;

Matches 12; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 12 LLVLGLWLALLRSVAGEQAPGTAP 35

Db 7 VLVVGLICAVFSSVGAQQAQAPSTSP 30

### RESULT 2

T34688

probable lipoprotein - Streptomyces coelicolor

C:Species: Streptomyces coelicolor

C>Date: 05-Nov-1999 #sequence\_revision 05-Nov-1999 #text\_change 09-Jul-2004

C:Accession: T34688

R:Harris, D.; Taylor, K.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, May 1998

A:Reference number: Z21553

A:Accession: T34688

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-289 <HAR>

A:Cross-references: UNIPROT:Q69838; EMBL:AL023517; PIDN:CAA18984.1; GSPDB:GN000070; SCORE

A:Experimental source: strain A3(2)

C:Genetics:

A:Gene: SCOREDB:SC1B5.10C

Query Match 32.4%; Score 55; DB 2; Length 289;

Best Local Similarity 46.7%; Pred. No. 7.7;

Matches 14; Conservative 2; Mismatches 14; Indels 0; Gaps 0;

Qy 6 LRRLLRLVLLGLWLALLRSVAGEQAPGTAP 35

Db 5 VRRATATCVLGAALAAACGTTGAEQAPRPAP 34

**RESULT 3**

Tl7480  
endo-xylanase homolog PCZA361.14 - Amycolatopsis orientalis  
C:Species: Amycolatopsis orientalis  
C>Date: 02-Sep-2000 #sequence\_revision 02-Sep-2000 #text\_change 09-Jul-2004  
C:Accession: Tl7480  
R;Van Wageningen, A.; Kirkpatrick, P.; Williams, D.; Harris, B.; Kershaw, J.; Lennard, N.  
Chem. Biol. 3, 155-162, 1998  
A>Title: Sequencing and analysis of genes involved in the biosynthesis of a vancomycin g  
A:Reference number: Z18804  
A:Accession: Tl7480  
A>Status: preliminary; translated from GB/EMBL/DDBB  
A:Molecule type: DNA  
A:Residues: 1-462 <VAN>  
A:Cross-references: UNIPROT:O52801; EMBL:AJ223998; NID:e1251208; PID:e1251219; PIDN:CAAI

Query Match 31.8%; Score 54; DB 2; Length 462;  
Best Local Similarity 44.8%; Pred. No. 16;  
Matches 13; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

**Qy** 6 LRLLRLVLGLWLALLRSVAGQAPGTA 34  
:|||||:|:|:|:|:|:|:  
**Db** 1 MRRLIALIVAGLALSVLAMPAAQAAPRAA 29

**RESULT 4**

C87609  
sensor histidine kinase, probable [imported] - Caulobacter crescentus  
C:Species: Caulobacter crescentus  
C>Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 09-Jul-2004  
C:Accession: C87609  
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.  
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon  
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.  
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
A>Title: Complete Genome Sequence of Caulobacter crescentus.  
A:Reference number: A87249; MUID:21173698; PMID:11259647  
A:Accession: C87609  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-556 <STO>  
A:Cross-references: UNIPROT:Q9A4C7; GB:AEO05673; NID:g13424529; PIDN:AAK24871.1; GSPDB:G  
C:Genetics:  
A:Gene: CC2909

Query Match 31.8%; Score 54; DB 2; Length 556;  
Best Local Similarity 80.0%; Pred. No. 18;  
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

**Qy** 10 LRLLVLGLWLALLRS 24  
:|||||||:|  
**Db** 293 LLLLVLGLWLALVYS 307

**RESULT 5**

JE0337  
Frizzled-1 protein - human  
C:Species: Homo sapiens (man)  
C>Date: 05-Feb-1999 #sequence\_revision 05-Feb-1999 #text\_change 09-Jul-2004  
C:Accession: JE0337  
R;Sagara, N.; Toda, G.; Hirai, M.; Terada, M.; Katoh, M.  
Biochem. Biophys. Res. Commun. 252, 117-122, 1998  
A>Title: Molecular cloning, differential expression, and chromosomal localization of hum  
A:Reference number: JE0337; MUID:95032814; PMID:9813155  
A:Accession: JE0337  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-647 <SAG>  
A:Cross-references: UNIPROT:Q9UPJ8; DDBJ:AB017363; NID:g3927882; PIDN:EAA34666.1; PID:G  
C:Superfamily: fruit fly frizzled protein

Query Match 31.8%; Score 54; DB 2; Length 647;

submitted to the Protein Sequence Database, February 2000

A:Reference number: Z24138  
A:Accession: T46923  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-499 <AAA>  
A:CROSS-references: UNIPROT:Q43292; EMBL:AL157437  
A:Experimental source: adult testis; clone DKF2p434E1512  
C:Genetics:  
A:Note: DKF2p434E1512.1

Query Match 30.6%; Score 52; DB 2; Length 499;  
Best Local Similarity 41.2%; Pred. No. 31;  
Matches 14; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

QY 2 ARGSLRLRLVLGLWLLALLRSVAGEAQPAP 35  
DB 255 AVGFLLVLGLKALELWMLQHEAGMGLPEPGAP 288

#### RESULT 9

F83622 Probable permease of ABC transporter PA0185 [imported] - Pseudomonas aeruginosa (strain

C:Species: Pseudomonas aeruginosa  
C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004

C:Accession: F83622  
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,

Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho

A:Reference number: A82950; MUID:20437337; PMID:10984043

A:Accession: F83622

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-538 <STO>

A:CROSS-references: UNIPROT:Q916U8; GB:AE004456; GB:AE004091; NID:g9946013; PIDN:AAG0357

A:Experimental source: strain PA01

C:Genetics:  
A:Gene: PA0185

Query Match 30.6%; Score 52; DB 2; Length 538;

Best Local Similarity 48.4%; Pred. No. 33;

Matches 15; Conservative 1; Mismatches 11; Indels 4; Gaps 1;

QY 5 SLRRLRLVLGLWLLALLRSVAGEAQPAP 35

DB 435 SLGEARVLRLGFWRRRLRLV----LPGAAP 461

#### RESULT 10

A47531

Glutamyl aminopeptidase (EC 3.4.11.7) - human

N:Alternate names: aminopeptidase A; differentiation antigen gp160

C:Species: Homo sapiens (man)

C:Date: 02-Jun-1995 #sequence\_revision 02-Jun-1995 #text\_change 09-Jul-2004

C:Accession: A47531; A48287

R:Li, L.; Wang, J.; Cooper, M.D.

Genomics 17, 657-664, 1993

A:Title: cDNA cloning and expression of human glutamyl aminopeptidase (aminopeptidase A)

A:Reference number: A47531; MUID:94063909; PMID:8244382

A:Accession: A47531

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-957 <LIA>

A:CROSS-references: UNIPROT:Q07075; GB:L12468; NID:G347892; PIDN:AAA16876.1; PID:G347893

R:Nanus, D.M.; Engelstein, D.; Gastl, G.A.; Gluck, L.; Vidal, M.J.; Morrison, M.; Finsta

Proc. Natl. Acad. Sci. U.S.A. 90, 7069-7073, 1993

A:Title: Molecular cloning of the human kidney differentiation antigen gp160: human amin

A:Reference number: A48287; MUID:93348214; PMID:8346219

A:Accession: A48287

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-217, 'A', 219-957 <NAN>  
A:CROSS-references: GB:L14721; NID:g291853; PIDN:AAA35522.1; PID:g291854  
C:Genetics:

A:Gene: GDB:ENPEP

A:CROSS-references: GDB:L38283; OMIM:L38297

A:Map position: 17pter-17p12

C:Superfamily: membrane alanyl aminopeptidase

C:Keywords: aminopeptidase; glycoprotein; transmembrane protein

Query Match 30.6%; Score 52; DB 2; Length 957;

Best Local Similarity 48.0%; Pred. No. 54;

Matches 12; Conservative 5; Mismatches 6; Indels 2; Gaps 1;

QY 13 LVGLWLLALLRSV--AGEQAFPTAP 35

DB 31 LIVGLAVGLTRSCDSSGDDGGPGTAP 55

#### RESULT 11

T02982

Probable sucrose transport protein - rice

C:Species: Oryza sativa (rice)

C:Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 09-Jul-2004

C:Accession: T02982

R:Hirose, T.; Imaizumi, N.; Scofield, G.N.; Furbank, R.T.; Ohsugi, R.

Plant Cell Physiol. 38, 1389-1396, 1997

A:Title: cDNA cloning and tissue specific expression of a gene for sucrose transporter f

A:Reference number: Z14809; MUID:98182940; PMID:9522469

A:Accession: T02982

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-537 <HTR>

A:CROSS-references: UNIPROT:O49838; EMBL:D87819; NID:g2723470; PIDN:BAA24071.1; PID:g272

A:Experimental source: cultivar Nipponbare, leaf

C:Genetics:

A:Gene: SUT1

C:Superfamily: common tobacco sucrose transport protein

Query Match 30.3%; Score 51.5; DB 2; Length 537;

Best Local Similarity 35.3%; Pred. No. 38;

Matches 12; Conservative 3; Mismatches 6; Indels 13; Gaps 1;

QY 14 VLGLWL-----ALLRSVAGEAQPATA 34

DB 169 VLGFLLDFSNNTVQGPAPALMADLSGRHGPGTA 202

#### RESULT 12

AD0753

flagellar biosynthetic protein Flp [imported] - Salmonella enterica subsp. enterica ser

C:Species: Salmonella enterica subsp. enterica serovar Typhi

A:Note: this species has also been called Salmonella typhi

C:Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002

C:Accession: AD0753

R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,

th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,

S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.,

A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov

A:Reference number: AB0502; MUID:21534947; PMID:11677608

A:Accession: AD0753

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-245 <PAR>

A:CROSS-references: GB:ALU513382; PIDN:CAD05727.1; PID:GL65032220; GSPDB:GN00176

C:Genetics:

A:Gene: STY2187

C:Superfamily: flagellar biosynthetic protein flp

Query Match 30.0%; Score 51; DB 2; Length 245;

Best Local Similarity 48.1%; Pred. No. 23;

Matches 13; Conservative 2; Mismatches 10; Indels 2; Gaps 1;

Qy 6 LRRLLRLVLGLWLLALLRSVAGEQAPG 32  
Db 1 MRRLLFLSLAGLW--LFSFAAAQLPG 25

## RESULT 13

S78698

probable export protein flip precursor - Salmonella typhimurium

C:Species: Salmonella typhimurium

C:Date: 01-Feb-1999 #sequence\_revision 01-Feb-1999 #text\_change 09-Jul-2004

C:Accession: S78698

R:Ohnishi, K.; Fan, F.; Schoenhals, G.J.; Kihara, M.; Macnab, R.M.

J. Bacteriol. 179, 6092-6099, 1997

A:Title: The FlpO, FlpP, and FlpR proteins of Salmonella typhimurium: putative com

A:Reference number: S78696; MUID:97464436; PMID:9324257

A:Accession: S78698

A:Molecule type: DNA

A:Residues: 1-245 &lt;OHN&gt;

A:Cross-references: UNIPROT:P54700; EMBL:L49021; NID:gl066860; PIDN:AA81319.1; PID:gl06

A:Note: the sequence of residues 42-241 and the corresponding nucleic acid sequence are

C:Genetics:

A:Gene: flip

C:Function:

A:Description: may be involved in flagellar assembly; may be involved in export of flag

C:Superfamily: flagellar biosynthetic protein flip

C:Keywords: flagellum; transmembrane protein

F:1-21/Domain: signal sequence #status predicted &lt;SIG&gt;

F:22-245/Product: probable export protein flip #status predicted &lt;MAT&gt;

F:45-61/Domain: transmembrane #status predicted &lt;TM1&gt;

F:89-105/Domain: transmembrane #status predicted &lt;TM2&gt;

F:189-205/Domain: transmembrane #status predicted &lt;TM3&gt;

F:212-228/Domain: transmembrane #status predicted &lt;TM4&gt;

Query Match 30.0%; Score 51; DB 2; Length 245;

Best Local Similarity 48.1%; Pred. No. 23;

Matches 13; Conservative 2; Mismatches 10; Indels 2; Gaps 1;

Qy 6 LRRLLRLVLGLWLLALLRSVAGEQAPG 32

Db 1 MRRLLFLSLAGLW--LFSFAAAQLPG 25

## RESULT 14

F75251

cytochrome C oxidase assembly factor - Deinococcus radiodurans (strain R1)

C:Species: Deinococcus radiodurans

C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004

C:Accession: F75251

R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;

S.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma

S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999

A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A:Reference number: A75250; MUID:20036896; PMID:10567266

A:Accession: F75251

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-313 &lt;WHI&gt;

A:Cross-references: UNIPROT:Q9RR78; GB:AE002091; GB:AE000513; NID:g6460446; PIDN:AAF1215

A:Experimental source: strain R1

C:Genetics:

A:Gene: DR2618

A:Map position: 1

C:Superfamily: heme O synthase

Query Match

Best Local Similarity 30.0%; Score 51; DB 2; Length 313;

Matches 10; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 16 GLWLLALLRSVAGEQAPGTA 34

Db 56 GLWLLIVVSVAGYMSAGSA 74

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2005, 18:01:53 ; Search time 50.1974 Seconds  
(without alignments)  
357.046 Million cell updates/sec

Title: US-10-062-831-59\_COPY\_1\_35

Perfect score: 170

Sequence: 1 MARGSLRLLRLVGLWLLRLSRVAGQAPGTAP 35

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt\_03:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	170	100.0	129	1	FN14 HUMAN
2	96	56.5	129	2	Q80X99 ratius norv
3	92	54.1	129	1	FN14 MOUSE
4	60	35.3	466	2	Q89W72 bradyrhizob
5	60	35.3	508	2	Q8W616 sinorhizobi
6	59	34.7	228	2	Q43558 medicago sa
7	59	34.7	401	2	Q97407 anopheles g
8	58	34.1	577	2	Q8S922 oryza sativ
9	58	34.1	577	2	Q6EU76 oryza sativ
10	58	34.1	577	2	Q6VEF4 oryza sativ
11	57	33.5	986	2	Q6L8S8 mus musculu
12	56	32.9	173	2	Q9JKD5 rattus norv
13	56	32.9	300	2	Q9JHY1 rattus norv
14	55	32.4	289	2	Q69838 streptomyce
15	55	32.4	300	2	Q8VC39 mus musculu
16	55	32.4	465	2	Q82B13 streptomyce
17	55	32.4	527	2	Q82A33 streptomyce
18	55	32.4	572	2	Q9W2P2 drosophila
19	55	32.4	873	2	Q98949 gallus gall
20	55	32.4	962	2	Q8Y055 ralstonia s
21	54.5	32.1	809	2	Q66DL4 versinia ps
22	54.5	32.1	823	2	Q8WY18 homo sapien
23	54.5	32.1	823	2	Q8CE84 mus musculu
24	54.5	32.1	1188	1	ITAH MOUSE
25	54.5	32.1	1188	2	Q7TQC3 mus musculu
26	54.5	32.1	1189	1	ITAH HUMAN
27	54	31.8	95	2	Q9AX04 oryza sativ
28	54	31.8	300	1	JAM1 MOUSE
29	54	31.8	401	2	Q7QFQ0 anopheles g
30	54	31.8	404	2	Q82C69 streptomyce
31	54	31.8	418	2	Q91AF4 bacillus sp

## RESULT 1

ID	FN14 HUMAN	STANDARD;	PRT;	129 AA.
AC	Q9NP84; Q9HCS0;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Tumor necrosis factor receptor superfamily member FN14 precursor			
DE	(Fibroblast growth factor-inducible immediate-early response protein			
DE	14) (TGF-inducible 14) (Tweak-receptor) (TweakR).			
GN	Name=TNFRSF12A; Synonyms=FN14;			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Placenta;			
RX	MEDLINE=20216634; PubMed=10751351;			
RA	Feng S.-L.Y., Guo Y., Factor V.M., Thorgerirsson S.S., Bell D.W.,			
RA	Testa J.R., Peifley K.A., Winkles J.A.;			
RT	"The FN14 immediate-early response gene is induced during liver			
RT	regeneration and highly expressed in both human and murine			
RT	hepatocellular carcinomas."			
RL	Am. J. Pathol. 156:1253-1261(2000).			
RL	[2]			
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).			
RA	Tanaka S., Sugimachi K.;			
RT	"Human homologue of FN14."			
RL	Submitted (DSC-1999) to the EMBL/GenBank/DBSJ databases.			
RL	[3]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Uterus;			
RX	MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shermen C.M., Schuler G.D.,			
RA	Altschuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalish D.B.,			
RA	Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			

052801 amycolatops  
Q62k31 burkholderi  
Q94c7 caulobacter  
Q9up38 homo sapien  
Q7n410 photornadu  
Q9m0s4 arabidopsis  
Q9ub33 anopheles g  
Q6aqm2 desulfotale  
Q8pj4 xanthomonas  
Q55364 synechocyst  
Q70i04 streptomyce  
Q758d4 ashbya goss  
Q8qvl2 hamster par  
Q94798 trypanosoma







```
RA Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
RT Bradyrhizobium japonicum USDA110.";
RL DNA Res. 9:189-197(2002).
DR EMBL; AF005937; BAC46086.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0015297; P:antiporter activity; IEA.
DR GO; GO:0015238; F:drug transporter activity; IEA.
DR GO; GO:0008655; P:multidrug transport; IEA.
DR InterPro; IPR002528; Mate; 2.
DR Pfam; PF01554; Mate; 2.
DR TIGRFAMs; TIGR00797; mate; 1.
KW Complete proteome.
SQ SEQUENCE 466 AA; 49216 MW; BBD66F41E70E694A CRC64;

Query Match 35.3%; Score 60; DB 2; Length 466;
Best Local Similarity 46.4%; Pred. No. 15;
Matches 13; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 4 GSLRLLRLVLGLWALLRSVAGEQAP 31
DB 97 GQVRRIRRALRVGLWVALLISLPWASP 124

RESULT 5
Q8W616 PRELIMINARY; PRT; 508 AA.
AC Q8W616;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein orf41.
GN Name=orf41;
OS Sinorhizobium meliloti phase PBC5.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales.
OX NCBI_TaxID=179237;
RN [1]
RP SEQUENCE FROM N.A.
RA Schulmeister S.A., Krol J.E., Vorhoelter F.-J., Skorupska A.M.,
RA Lotz W.;
RT "Sequence of the genome of Sinorhizobium meliloti bacteriophage
RT PBC5.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Schulmeister S.A., Krol J.E., Vorhoelter F.-J., Skorupska A.M.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF448724; AAL49639.1; -.
KW Hypothetical protein.
SQ SEQUENCE 508 AA; 54579 MW; C61CE7A54EF600F5 CRC64;

Query Match 35.3%; Score 60; DB 2; Length 508;
Best Local Similarity 51.5%; Pred. No. 16;
Matches 17; Conservative 4; Mismatches 8; Indels 4; Gaps 1;

QY 4 GSLRLLRLVLGLWALLR---SVAGEQAPG 32
DB 248 GGLRLLRLLLRLLLCLVGLCCCSILLGRRAHG 280

RESULT 6
Q43558 PRELIMINARY; PRT; 228 AA.
AC Q43558;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Proline rich protein precursor.
OS Medicago sativa (Alfalfa).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.
OX NCBI_TaxID=3879;
```

```
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Stem;
RX MEDLINE=95201245; PubMed=7894016;
RA Abrahams S., Hayes C.M., Watson J.M.;
RT "Expression patterns of three genes in the stem of lucerne (Medicago
RT sativa).";
RL Plant Mol. Biol. 27:513-528(1995).
DR EMBL; L36120; AAB41815.1; -.
DR PIR; S53504; S53504.
KW Signal.
FT SIGNAL 1 7 potential.
FT CHAIN 8 228 proline rich protein.
SQ SEQUENCE 228 AA; 22480 MW; 15CAA63CC1F0532E CRC64;

Query Match 34.7%; Score 59; DB 2; Length 228;
Best Local Similarity 50.0%; Pred. No. 10;
Matches 12; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 12 LLVLGLWALLRSVAGEQAPGTAP 35
DB 7 VLVVGLICAVFSSVGAQAPSTSP 30

RESULT 7
Q97407 PRELIMINARY; PRT; 401 AA.
AC Q97407;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE SGI protein precursor.
GN Name=SGI;
OS Anopheles gambiae (African malaria mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=7165;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GASUA; TISSUE=Salivary gland;
RX MEDLINE=99145581; PubMed=990055; DOI=10.1073/pnas.96.4.1516;
RA Arca B., Lombardo F., de Lara Capurro M., della Torre A.,
RA Dinopoulos G., James A.A., Coluzzi M.;
RT "Trapping cDNAs encoding secreted proteins from the salivary glands of
RT the malaria vector Anopheles gambiae.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:1516-1521(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=GASUA; TISSUE=Salivary gland;
RA Arca' B., Lombardo F., Capurro de Lara Guimaraes M., della Torre A.,
RA Dinopoulos G., James A.A., Coluzzi M.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ130949; CAA10258.1; -.
KW Signal.
FT SIGNAL 1 14
SQ SEQUENCE 401 AA; 46277 MW; 22000EAB25CE8085 CRC64;

Query Match 34.7%; Score 59; DB 2; Length 401;
Best Local Similarity 55.0%; Pred. No. 17;
Matches 11; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 10 LRLLVLGLWALLRSVAGEQ 29
DB 1 MRLLVLTINIGCVNSTFGEQ 20

RESULT 8
Q8S922 PRELIMINARY; PRT; 577 AA.
AC Q8S922;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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DE Cell wall invertase (EC 3.2.1.26).  
GN Name=Oscini;  
OS Oryza sativa (japonica cultivar-group).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzaceae; Oryza.  
OX NCBI\_TaxID=39947;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Panicum;  
RX MEDLINE=21975747; PubMed=11978873;  
RA Hirose T.; Takano M.; Terao T.;  
RT "Cell wall invertase in developing rice caryopsis: molecular cloning  
of Oscini and analysis of its expression in relation to its role in  
grain filling."  
RL Plant Cell Physiol. 43:452-459(2002).  
CC 1- SIMILARITY: Belongs to family 32 of glycosyl hydrolases.  
DR EMBL: AB073749; BAB90855.1; -;  
DR Gramine; Q8S922; -;  
DR GO: GO:0004564; F:beta-fructofuranosidase activity; IEA.  
DR GO: GO:0005975; P:carbohydrate metabolism; IEA.  
DR InterPro: IPR001362; Glyco\_hydro\_32.  
DR InterPro: IPR011040; Sialidase.  
DR Pfam: PF00251; Glyco\_hydro\_32; 1.  
DR SMART: SM00640; Glyco\_32; 1.  
DR PROSITE: PS00609; GLYCOSYL\_HYDROL\_F32; 1.  
KW Glycosidase; Hydrolase.  
SQ SEQUENCE 577 AA; 63984 MW; 41PE6384284F97F1 CRC64;  
  
Query Match 34.1%; Score 58; DB 2; Length 577;  
Best Local Similarity 40.5%; Pred. No. 33;  
Matches 15; Conservative 2; Mismatches 8; Indels 12; Gaps 1;  
  
QY 11 RLLVLGLWLLAL-----RSVAGEQAPGTAP 35  
Db 4 RLLALAPWLLLLLLQLAGASHVHRSLEAEQAPSSVP 40  
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RESULT 9  
Q6EU76 PRELIMINARY; PRT; 577 AA.  
ID Q6EU76;  
AC Q6EU76;  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Cell wall invertase 1.  
GN Name=OJ112.G07.1; Synonyms=B1136H02.14;  
OS Oryza sativa (japonica cultivar-group).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzaceae; Oryza.  
OX NCBI\_TaxID=39947;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Sasaki T.; Matsumoto T.; Katayose Y.;  
RL Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.  
CC 1- SIMILARITY: Belongs to family 32 of glycosyl hydrolases.  
DR EMBL: AP004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.  
DR GO: GO:0004564; P:carbohydrate metabolism; IEA.  
DR InterPro: IPR001362; Glyco\_hydro\_32.  
DR InterPro: IPR011040; Sialidase.  
DR Pfam: PF00251; Glyco\_hydro\_32; 1.  
DR SMART: SM00640; Glyco\_32; 1.  
DR PROSITE: PS00609; GLYCOSYL\_HYDROL\_F32; 1.  
KW Glycosidase; Hydrolase.  
SQ SEQUENCE 577 AA; 63984 MW; 2A39D555E834529C CRC64;

Query Match 34.1%; Score 58; DB 2; Length 577;  
Best Local Similarity 40.5%; Pred. No. 33;  
Matches 15; Conservative 2; Mismatches 8; Indels 12; Gaps 1;  
  
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Db 4 RLLALAPWLLLLLLQLAGASHVHRSLEAEQAPSSVP 40  
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ID Q6VEF4;  
AC Q6VEF4;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Cell wall invertase 1 (EC 3.2.1.26).  
GN Name=CIN1;  
OS Oryza sativa (indica cultivar-group).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzaceae; Oryza.  
OX NCBI\_TaxID=39946;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Wang Y.-Q.; Zhu Z.;  
RL Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.  
CC 1- SIMILARITY: Belongs to family 32 of glycosyl hydrolases.  
DR EMBL: AY342319; AAQ24869.1; -;  
DR GO: GO:0004564; F:beta-fructofuranosidase activity; IEA.  
DR GO: GO:0005975; P:carbohydrate metabolism; IEA.  
DR InterPro: IPR001362; Glyco\_hydro\_32.  
DR InterPro: IPR011040; Sialidase.  
DR Pfam: PF00251; Glyco\_hydro\_32; 1.  
DR SMART: SM00640; Glyco\_32; 1.  
DR PROSITE: PS00609; GLYCOSYL\_HYDROL\_F32; 1.  
KW Glycosidase; Hydrolase.  
SQ SEQUENCE 577 AA; 63984 MW; 2A39D555E834529C CRC64;  
  
Query Match 34.1%; Score 58; DB 2; Length 577;  
Best Local Similarity 40.5%; Pred. No. 33;  
Matches 15; Conservative 2; Mismatches 8; Indels 12; Gaps 1;  
  
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Db 4 RLLALAPWLLLLLLQLAGASHVHRSLEAEQAPSSVP 40  
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RESULT 11  
Q6L8S8 PRELIMINARY; PRT; 986 AA.  
ID Q6L8S8;  
AC Q6L8S8;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Beta1,4-N-acetylgalactosaminyltransferase III.  
GN Name=beta4GalNACT3;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX PubMed=12966086; DOI=10.1074/jbc.M308857200;  
RA Sato T.; Gotoh M.; Kiyohara K.; Kameyama A.; Kubota T.; Kikuchi N.;  
RA Ishizuka Y.; Iwasaki H.; Togayachi A.; Kudo T.; Ohkura T.;  
RA Nakanishi H.; Narimatsu H.;  
RT "Molecular cloning and characterization of a novel human beta 1,4-N-  
acetylgalactosaminyltransferase, beta 4GalNAC-T3, responsible for the  
synthesis of N,N'-diacetyllactosamine, galNAC beta 1-4GlcNAc.";  
RL J. Biol. Chem. 278:47534-47544(2003).  
DR EMBL: AB114826; BAD02450.1; -;  
DR GO: GO:0016740; F:transferase activity; IEA.

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,  
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 Fahey J., Heiton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,  
 Krzywinski M.I., Skaleka U., Smalilus D.E., Schnurch A., Schein J.E.,  
 Jones S.J., Marra M.A.  
 "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).  
 [3]  
 SEQUENCE FROM N.A.  
 RN TISSUE=Prostate;  
 RC Strausberg R.;  
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF276998; AAF78250.1; -;  
 DR EMBL; BC065309; AAF65309.1; -;  
 DR HSSP; O88792; 1F97.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; ig; 2.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG\_LIKE; 2.  
 SQ SEQUENCE 300 AA; 32369 MW; 45AF362A96158BFA CRC64;

Query Match 32.9%; Score 56; DB 2; Length 300;  
 Best Local Similarity 44.4%; Pred. No. 33;  
 Matches 12; Conservative 2; Mismatches 13; Indels 0; Gaps 0;

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 DB 249 LLGLLFIWFWAYSRGYFRTKKGATP 275  
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RESULT 14  
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 AC O69838;  
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 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)  
 DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DT Putative lipoprotein.  
 GN ORFNames=SCIB5.10c;  
 OS Streptomyces coelicolor.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Streptomycineae; Streptomycetaceae; Streptomyces.  
 OX NCBI\_TaxID=1902;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A3(2) / M145;  
 RX MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;  
 RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,  
 Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,  
 Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,  
 Cronin A., Fraser A., Goble A., Hidalgo J., Hornaby T., Howarth S.,  
 Huang C.-H., Kleser T., Lark L., Murphy L.D., Oliver K., O'Neill S.,  
 Rabinowitz B., Rajandream M.A., Rutherford K.M., Rutter S.,  
 Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,  
 Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,  
 Hopwood D.A.;  
 "Complete genome sequence of the model actinomycete Streptomyces  
 coelicolor A3(2).";  
 Nature 417:141-147(2002).  
 RL EMBL; AL339126; CAA18984.1; -;  
 DR F1R; T34688; T34688.  
 DR GO; GO:0016810; F:hydrolase activity, acting on carbon-nitrog. .; IEA.

DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
 DR InterPro; IPR002509; Polysac deacet.  
 DR Pfam; PF01522; Polysacc deac 1; 1.  
 KW Complete proteome; Lipoprotein.  
 SQ SEQUENCE 289 AA; 30748 MW; 4484081584FCD307 CRC64;  
 Query Match 32.4%; Score 55; DB 2; Length 289;  
 Best Local Similarity 46.7%; Pred. No. 44;  
 Matches 14; Conservative 2; Mismatches 14; Indels 0; Gaps 0;  
 QY 6 LRLRLLLVLGLWLLALLRSVAGEQAPGTAP 35  
 DB 5 VRRATALCVLGAALAAACGTTGAQPRAP 34  
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 AC Q8VC39;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE F11r protein (Mus musculus adult male cecum CDNA, RIKEN full-length  
 DE enriched library, clone:9130004G24 product:junction cell adhesion  
 DE molecule1, full insert sequence).  
 GN Name=F11r;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=mix FVB/N; TISSUE=Mammary tumor;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeng B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.P., Jordan M., Moore T., Max S.I., Wang J., Hsieh P.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=mix FVB/N; TISSUE=Mammary tumor;  
 RA Strausberg R.;  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Cecum;  
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
 RA Carninci P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning.";  
 RL Meth. Enzymol. 303:19-44 (1999).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Cecum;  
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
 RA RIKEN FANTOM Consortium;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690 (2001).

RN [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Cecum;  
 RA The FANTOM Consortium;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs.";  
 RL Nature 420:563-573 (2002).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Cecum;  
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
 RL Genome Res. 10:1617-1630 (2000).  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Cecum;  
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
 RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,  
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format  
 RT sequencing pipeline with 384 multipillar sequencer.";  
 RL Genome Res. 10:1757-1771 (2000).  
 RN [8]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Cecum;  
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
 RA Saito K., Satoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
 RA Tagawa A., Takahashi F., Takaku-Akaira S., Takeda Y., Tanaka T.,  
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC021876; AAH21876.1; -.  
 DR EMBL; AK033574; BAC28369.1; -.  
 DR HSSP; O88792; 1F97.  
 DR MGD; MGI:1321398; F11r.  
 DR GO; GO:0005615; C:extracellular space; TAS.  
 DR GO; GO:0016021; C:integral to membrane; TAS.  
 DR GO; GO:0005515; F:protein binding; IPI.  
 DR Pfam; PF00047; Ig; 2.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG LIKE; 2.  
 SQ SEQUENCE 300 AA; 32423 MW; 3CE561E8FF3B97EC CRC64;

Query Match 32.4%; Score 55; DB 2; Length 300;  
 Best Local Similarity 44.4%; Pred. No. 45;  
 Matches 12; Conservative 2; Mismatches 13; Indels 0; Gaps 0;

QY 9 LRLRLVLGLWLLALLRSVAGEQAPGTAP 35  
 DB 249 LLGLLIFGVWFAYSGYFERTKGTAP 275

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GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: February 10, 2005, 17:53:53 ; Search time 55.5702 Seconds  
(without alignments)  
243.595 Million cell updates/sec

Title: US-10-062-831-59\_COPY\_1\_35

Perfect score: 170

Sequence: 1 MARGSLRLRLLLVLGLMLALRLSVAGPQGTAP 35

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 385760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	170	100.0	112	3	AAY91463 Human sec
2	170	100.0	112	6	ADA57390 Human sec
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4	170	100.0	112	7	ADD38025 Human sec
5	170	100.0	112	8	ADL71535 Novel hum
6	170	100.0	114	2	AAW73409 Human sec
7	170	100.0	129	2	AAW88506 Human liv
8	170	100.0	129	3	AAW57940 Human tra
9	170	100.0	129	4	AAU03498 Human TWE
10	170	100.0	129	5	ABP61512 Human NP-
11	170	100.0	129	5	AAU79827 Human typ
12	170	100.0	129	6	ADA56889 Human sec
13	170	100.0	129	6	ABU56716 Lung canc
14	170	100.0	129	7	ADC74112 Human sec
15	170	100.0	129	7	ADD37867 Human sec
16	170	100.0	129	7	ADD89033 TAT274.1
17	170	100.0	129	7	ABU64232 Human FFA
18	170	100.0	129	7	ADN39126 Cancer/an
19	170	100.0	129	7	ADN39987 Cancer/an
20	170	100.0	129	8	ABM81706 Tumour-as
21	170	100.0	155	3	AAW91604 Human sec
22	170	100.0	155	6	ADA57391 Human sec
23	170	100.0	155	7	ADC74463 Human sec
24	170	100.0	155	7	ADD38026 Human sec
25	170	100.0	155	8	ADL71680 Novel hum

26	170	100.0	156	3	AAY91552 Human sec
27	170	100.0	156	8	ADL71624 Novel hum
28	170	100.0	309	4	AAU03500 Human TWE
29	158	92.9	94	7	ABU64233 Human CRY
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31	61	35.9	79	5	ABP06392 Human ORF
32	57	33.5	986	8	ADK43170 Mouse N-a
33	56.5	33.2	671	6	ABU31710 Protein e
34	55	32.4	300	8	ADR46581 Mouse jun
35	55	32.4	572	4	ABT70909 Drosophil
36	54.5	32.1	1120	6	ABT58365 Human NOV
37	54.5	32.1	1188	4	AAU14467 Human nov
38	54.5	32.1	1188	4	AAU14231 Human nov
39	54.5	32.1	1188	4	AAU50085 Human A25
40	54.5	32.1	1188	4	AAU50087 Murine A2
41	54.5	32.1	1188	5	AAU10552 Murine A2
42	54.5	32.1	1188	5	AAU10551 Human A25
43	54.5	32.1	1188	7	ADE09956 Novel pro
44	54.5	32.1	1189	3	AAU25582 ITGA11 pr
45	54.5	32.1	1189	4	ABG12949 Novel hum

ALIGNMENTS

RESULT 1  
AAY91463  
ID AAY91463 standard; protein; 112 AA.  
XX AC AAY91463;  
XX AC  
XX 29-JUN-2000 (first entry)  
XX DE Human secreted protein sequence encoded by gene 13 SEQ ID NO:136.  
XX KW Human; secreted protein; diagnosis; cytostatic; immunosuppressive;  
XX KW antiHIV; antiinflammatory; nootropic; neuroprotective; antiallergic;  
XX KW osteopathic; antiarthritic; antibacterial; antidiabetic; antiaslthma;  
XX KW antipsoriatic; cardiant; gene therapy; cancer; neurological disorder;  
XX KW immune disease; inflammation; blood disorder; tumour; chromosome 16.  
XX OS Homo sapiens.  
XX PN WO200006698-A1.  
XX PD 10-FEB-2000.  
XX PF 29-JUL-1999; 99WO-US017130.  
XX PR 30-JUL-1998; 98US-0094657P.  
XX PR 05-AUG-1998; 98US-0095486P.  
XX PR 06-AUG-1998; 98US-0095454P.  
XX PR 06-AUG-1998; 98US-0095455P.  
XX PR 12-AUG-1998; 98US-0096319P.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX PA  
XX PI Komatsoulis GA, Rosen CA, Ruben SM, Duan R, Moore PA, Shi Y;  
XX PI Lafleur D, Wei Y, Ni J, Florence KA, Young PE, Brewer LA;  
XX PI Soppet DR, Endress GA, Ebner R, Olsen HS, Mucenski M;  
XX DR WPI, 2000-195282/17.  
XX DR N-PSDB; AAA26358.  
XX PT New isolated human genes and the secreted polypeptides they encode,  
XX PT useful for diagnosis and treatment of e.g. cancers, neurological  
XX PT disorders, immune diseases, inflammation or blood disorders.  
XX PS Claim 11; Page 465; 634pp; English.

The polynucleotide sequences given in AAA26346 to AAA26458 encode the human secreted proteins given in AAY91451 to AAY91691. The human secreted proteins can have activities based on the tissues and cells they are

expressed in. Examples of the activities are: cytostatic; immunosuppressive; antiviral; antiinflammatory; neurotropic; neuroprotective; antiasthmatic; osteopathic; antiarthritic; antibacterial; antidiabetic; antiasthma; antiparasitic; and cardiant. The polynucleotides and their corresponding secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the proteins in a sample or by determining the presence of mutations in the polynucleotides. Specific uses are described for each of the polynucleotides, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, neurodegenerative disorders, developmental abnormalities and foetal deficiencies, blood disorders, diseases of the immune system, autoimmune diseases, hepatic and renal disease, inflammation, allergies, Alzheimer's and behavioural disorders, schizophrenia, osteoporosis, arthritis, infections, AIDS, spinal cord injuries, transplant rejection, diabetes, asthma, sepsis, acne, psoriasis, cardiovascular disorders, reproductive disorders, gastrointestinal disorders, respiratory disorders and metabolic disorders. The proteins or polynucleotides can also be used as food additives or preservatives. The proteins are also useful for identifying their binding partners. AAA26337 to AAA26345 and AAY91450 are sequences used in the exemplification of the present invention

Sequence 112 AA;  
Query Match 100.0%; Score 170; DB 3; Length 112;  
Best Local Similarity 100.0%; Pred. No. 3.1e-16;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARGSLRRLRLVLGLWLALLRSVAGEQAPGTAP 35  
|||||  
Db 1 MARGSLRRLRLVLGLWLALLRSVAGEQAPGTAP 35

## RESULT 2

ADA57390  
ID ADA57390 standard; protein; 112 AA.

XX ADA57390;

DT 20-NOV-2003 (first entry)

XX Human secreted protein #172.

XX immunosuppressive; antiinflammatory; antiasthmatic; antiasthmatic; antiallergic;  
KW cytostatic; cerebroprotective; neuroprotective; neurotropic;  
KW cardiovascular; antiarteriosclerotic; gene therapy;  
KW human secreted protein; immune disorder; inflammation;  
KW respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;  
KW inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;  
KW multiple sclerosis; ischaemic brain injury; Parkinson's disease;  
KW Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;  
KW triple helix formation; antisense gene therapy; forensic biology.

XX Homo sapiens.

XX WO2002102994-A2.

XX 27-DEC-2002.

XX 19-MAR-2002; 2002WO-US008278.

XX 21-MAR-2001; 2001US-0277340P.

XX 19-JUL-2001; 2001US-0306171P.

XX 13-NOV-2001; 2001US-0331287P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM;

XX WPI; 2003-167512/16.

XX N-PSDB; ADA56496.

XX

PT New human secreted polypeptides and polynucleotides, useful for  
PT diagnosing, treating or preventing e.g. immune disorders, inflammatory  
PT conditions, respiratory disorders, cancers, CNS disorders, or  
PT neurodegenerative disorders.

PS Claim 13; SEQ ID NO 1582; 1754pp; English.

XX The invention relates to 592 new human secreted polypeptides useful for  
CC diagnosing, treating or preventing e.g. immune disorders, inflammatory  
CC conditions, respiratory disorders, cancers, CNS disorders, or  
CC neurodegenerative disorders, or polypeptides comprising an amino acid  
CC sequence at least 95% identical to the new sequences. The polypeptides,  
CC antibodies or antibody fragments that bind to the polypeptides, nucleic  
CC acids encoding the polypeptides, agonists or antagonists that binds to  
CC the polypeptide, are useful in preparing diagnostic or pharmaceutical  
CC compositions for diagnosing, treating or preventing an e.g. immune  
CC disorders, inflammatory conditions (e.g. inflammatory bowel disease,  
CC nephritis or Crohn's disease), respiratory disorders (e.g. asthma and  
CC allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders  
CC (e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative  
CC disorders (e.g. Parkinson's disease or Alzheimer's disease), and  
CC cardiovascular disorders (e.g. atherosclerosis or myocarditis). The  
CC polynucleotides are useful for chromosome identification, chromosome  
CC mapping, for controlling gene expression through triple helix formation  
CC or antisense DNA or RNA, in gene therapy, for identifying individuals  
CC from minute biological samples, in forensic biology, and as hybridization  
CC probes. The polypeptides are useful for as molecular weight markers on  
CC sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE)  
CC gels, to raise antibodies, for testing biological activities, and for  
CC treating or preventing neural disorders, immune system disorders,  
CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,  
CC renal, proliferative and/or cancerous diseases. This sequence corresponds  
CC to one of the polypeptide of the invention. Note: The sequence data for  
CC this patent did form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 112 AA;

Query Match 100.0%; Score 170; DB 6; Length 112;

Best Local Similarity 100.0%; Pred. No. 3.1e-16;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARGSLRRLRLVLGLWLALLRSVAGEQAPGTAP 35

Db 1 MARGSLRRLRLVLGLWLALLRSVAGEQAPGTAP 35

## RESULT 3

ADC74462

ID ADC74462 standard; protein; 112 AA.

XX ADC74462;

XX 01-JAN-2004 (first entry)

XX Human secreted protein - SEQ ID 1095.

XX antianemic; antirheumatic; antiarthritic; antiinflammatory; antithyroid;  
KW antidiabetic; immunosuppressive; dermatological; nephrotropic;  
KW antiparkinsonian; neuroprotective; neurotropic; antibacterial; virucide;  
KW fungicide; antiparasitic; antiarteriosclerotic; vulnerary; cytostatic;  
KW haemopoietic; haematologic; anaemia; autoimmune disorder;  
KW rheumatoid arthritis; inflammation; Grave's disease; diabetes;  
KW systemic lupus erythematosus; glomerulonephritis; neurodegenerative;  
KW Parkinson's; Alzheimer's; wound; hyperproliferative; atherosclerosis;  
KW cancer; bacterial; viral; fungal; parasitic infection; gene therapy;  
KW human.

XX Homo sapiens.

XX WO2003038063-A2.

XX





```
OS Homo sapiens.
XX US2004034196-A1.
XX 19-FEB-2004.
XX
XX 27-JAN-2003; 2003US-00351334.
XX
XX 30-JUL-1998; 98US-0094657P.
XX 05-AUG-1998; 98US-0095486P.
XX 06-AUG-1998; 98US-0095454P.
XX 06-AUG-1998; 98US-0095455P.
XX 12-AUG-1998; 98US-0096319P.
XX 29-JUL-1999; 99WO-US017130.
XX 24-JAN-2000; 2000US-00489847.
XX 25-JAN-2002; 2002US-0350898P.
XX
XX (KOMA/) KOMATSOUKIS G A.
XX (ROSE/) ROSEN C A.
XX (RUBE/) RUBEN S M.
XX (DUAN/) DUAN D R.
XX (MOOR/) MOORE P A.
XX (SHIY/) SHI Y.
XX (LAFLE/) LAFLEUR D W.
XX (WEIY/) WEI Y.
XX
XX Komatsoulis GA, Rosen CA, Ruben SM, Duan DR, Moore PA, Shi Y;
XX Laflaur DW, Wei Y;
XX WPI; 2004-180094/17.
XX N-PSDB; ADL71419.
XX
XX New human secreted nucleic acid, useful for diagnosing and treating
XX neurodegenerative, inflammatory, hyperproliferative, metabolic,
XX reproductive, cardiovascular, respiratory or immunological disorders or
XX diseases.
XX
XX Claim 11; SEQ ID NO 139; 234pp; English.
XX
XX The invention describes an isolated human nucleic acid molecule (1)
XX comprising a polynucleotide having a nucleotide sequence at least 95%
XX identical to: a sequence polynucleotide fragment of SEQ ID NO: X or of
XX the cDNA sequence included in ATCC Deposit No: Z, which is hybridisable
XX to SEQ ID NO: X; or a sequence encoding a polypeptide fragment, domain or
XX epitope of SEQ ID NO: Y or a polypeptide sequence encoded by the cDNA
XX sequence included in ATCC Deposit No: Z, which is hybridisable to SEQ ID
XX NO: X, having a biological activity. The nucleic acids and polypeptides,
XX pharmaceutical formulations and kits are useful in diagnosing and
XX treating neurodegenerative diseases states, behavioral disorders,
XX inflammatory conditions, hyperproliferative disorders (e.g. Alzheimer's
XX disease, Parkinson's disease or Huntington's disease), metabolic
XX disorders (e.g. Tay-Sachs disease or Leish-Nyman syndrome), reproductive
XX disorders, immunological disorders (e.g. arthritis, asthma or AIDS),
XX endocrine and immune disorders (e.g. Hodgkin's lymphoma), haematopoietic
XX or muscular disorders (e.g. leukaemia), autoimmune disorders, allergy,
XX cancer, cardiovascular, respiratory or pulmonary disorders, disorders or
XX conditions afflicting connective tissue, skin disorders, CNS disorders,
XX congenital disorders, infectious disorders and gastrointestinal
XX disorders. This is the amino acid sequence of a novel human secreted
XX protein of the invention. Note: This sequence does not appear in the
XX printed specification but is available in electronic format from the US
XX patent office at ftp.segdata.uspto.gov/segdata.html?DocID=20040034196.
XX
XX Sequence 112 AA;
XX
XX Query Match 100.0%; Score 170; DB 8; Length 112;
XX Best Local Similarity 100.0%; Pred. No. 3.1e-16;
XX Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MARGSLRLLLVGLVGLVLLRSLVAGSQAGCTAP 35
XX |||||
XX 1 MARGSLRLLLVGLVGLVLLRSLVAGSQAGCTAP 35
XX |||||
XX
XX RESULT 6
XX AAW73409
XX ID AAW73409 standard; protein; 114 AA.
XX
XX AC AAW73409;
XX
XX DT 19-FEB-1999 (first entry)
XX
XX Human secreted protein encoded by Gene No. 13.
XX
XX Secreted protein; human; protein therapy; gene therapy; blood disorder;
XX pathological condition; diagnosis; cancer; neurological disorder;
XX developmental abnormality; foetal deficiency; leukaemia; hepatic disease;
XX immune system disorder; Alzheimer's disease; cognitive disorder;
XX schizophrenia; prostate disease; autoimmune disorder; AIDS.
XX
XX OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX Misc-difference 114 /note= "unspecified amino acid"
XX
XX WO9854206-A1.
XX
XX 03-DEC-1998.
XX
XX 28-MAY-1998; 98WO-US010868.
XX
XX 30-MAY-1997; 97US-0044039P.
XX 30-MAY-1997; 97US-0048093P.
XX 30-MAY-1997; 97US-0048101P.
XX 30-MAY-1997; 97US-0048190P.
XX 30-MAY-1997; 97US-0048356P.
XX 30-MAY-1997; 97US-0050935P.
XX 29-AUG-1997; 97US-0056250P.
XX 29-AUG-1997; 97US-0056293P.
XX 29-AUG-1997; 97US-0056296P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Rosen CA, Carter KC, Dillon PU, Endress GA, Yu G;
XX Ni J, Feng P;
XX WPI; 1999-070209/06.
XX N-PSDB; AAV08823.
XX
XX New isolated human genes - useful for diagnosis and treatment of, e.g.
XX cancers, neurological disorders, immune diseases, developmental disorders
XX or blood disorders.
XX
XX Claim 11; Page 153; 188pp; English.
XX
XX This sequence is encoded by a cDNA of the invention, designated Gene No.
XX 13. This sequence represents a human secreted protein, and is expressed
XX in keratinocytes and to a lesser extent in endothelial cells and
XX placenta. The DNA sequences of the invention and their corresponding
XX secreted polypeptides are useful for preventing, treating or ameliorating
XX medical conditions, e.g. by protein or gene therapy. Also pathological
XX conditions can be diagnosed by determining the amount of the new
XX polypeptides in a sample or by determining the presence of mutations in
XX the DNA sequences. Specific uses are described for each of the DNA
XX sequences and the encoded proteins, based on which tissues they are most
XX highly expressed in, and include developing products for the diagnosis or
XX treatment of cancer, tumours, neurological disorders, developmental
XX abnormalities and foetal deficiencies, blood disorders, leukaemias,
XX diseases of the immune system (including allergies or asthma), hepatic
XX diseases, Alzheimer's and cognitive disorders, schizophrenia, prostate
XX diseases, autoimmune disorders and AIDS. The polypeptides are also useful
XX for identifying their binding partners
XX
XX Sequence 114 AA;
```

```
Query Match      100.0%; Score 170; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 3.1e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARGSLRLLRLVLLGLWLLALLRSVAGEQAPGTAP 35
DB 1 MARGSLRLLRLVLLGLWLLALLRSVAGEQAPGTAP 35

RESULT 7
AAW88506
ID AAW88506 standard; protein; 129 AA.
AC AAW88506;
XX
XX
DT 30-MAR-1999 (first entry)
DE
DE Human liver clone HP10432-encoded membrane protein.
KW Transmembrane protein; HP10432; human; liver.
OS Homo sapiens.
XX
XX WO9855508-A2.
XX
XX 10-DEC-1998.
XX
XX 03-JUN-1998; 98WO-JP002445.
XX
XX 03-JUN-1997; 97JP-00144948.
XX
XX (SAGA ) SAGAMI CHEM RES CENTRE.
XX (PROT-) PROTEGENE INC.
XX
XX Kato S, Sekine S, Yamaguchi T;
XX WPI; 1999-045730/04.
XX N-PSDB; AAV84374.
XX
XX New human proteins containing transmembrane domains and their encoding
XX sequences - useful in the preparation of antibodies and large-scale
XX protein production, gene diagnosis, and gene therapy.
XX
XX Claim 1; Page 152-153; 178pp; English.
XX
XX This is the amino acid sequence of a transmembrane protein encoded by
XX human liver cDNA clone HP10432 (see AAV84374). The encoded protein has a
XX signal-like N-terminal region and one internal transmembrane domain. The
XX invention provides nucleotide sequences (see AAV84359-76) coding for 18
XX transmembrane proteins (see AAW88491-508), vectors containing such
XX polynucleotides, and eukaryotic cells containing the vectors. The
XX proteins can be used as antigens or as compositions in the preparation of
XX antibodies against the proteins. The polynucleotides can be used as
XX probes for gene diagnosis, and as gene sources for gene therapy and large
XX scale production of proteins encoded by the cDNA. The host cells are
XX used for the detection of ligands corresponding to the expressed
XX proteins, and the screening of low mol.wt. medicines
XX
XX Sequence 129 AA;

Query Match      100.0%; Score 170; DB 2; Length 129;
Best Local Similarity 100.0%; Pred. No. 3.5e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARGSLRLLRLVLLGLWLLALLRSVAGEQAPGTAP 35
DB 1 MARGSLRLLRLVLLGLWLLALLRSVAGEQAPGTAP 35

RESULT 8
AAV57940
ID AAV57940 standard; protein; 129 AA.
XX
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```
AC AAY57940;
XX
XX 23-MAR-2000 (first entry)
XX
XX Human transmembrane protein HTMPN-64.
XX
XX Human; transmembrane protein; HTMPN; diagnosis; immunospecific;
XX antiproliferative; neuroprotective; immune disorder;
XX reproductive disorder; smooth muscle disorder; neurological disorder;
XX gastrointestinal disorder; developmental disorder;
XX cell proliferative disorder.
XX
XX Homo sapiens.
XX OS
XX WO9961471-A2.
XX
XX 02-DEC-1999.
XX
XX 28-MAY-1999; 99WO-US011904.
XX
XX 29-MAY-1998; 98US-0087260P.
XX 02-JUL-1998; 98US-0091674P.
XX 02-OCT-1998; 98US-0102954P.
XX 24-NOV-1998; 98US-0109869P.
XX
XX (INCY-) INCYTE PHARM INC.
XX
XX Tang YT, Lal P, Hillman JL, Yue H, Guegler KJ, Corley NC;
XX Bandman O, Patterson C, Gorgone GA, Kaser MR, Baughn MR, Au-Young J;
XX WPI; 2000-072605/06.
XX N-PSDB; AAZ56761.
XX
XX Proteins, polynucleotides, vectors, host cells and antibodies used to
XX diagnose, treat or prevent immune, reproductive, smooth muscle,
XX neurological, gastrointestinal, developmental and cell proliferative
XX disorders.
XX
XX Claim 1; Page 163; 229pp; English.
XX
XX AAZ56698 to AAZ56776 encode AAY57877 to AAY57955 which represent human
XX transmembrane proteins designated HTMPN-1 to HTMPN-79, respectively. The
XX transmembrane protein have immunospecific, antiproliferative and
XX neuroprotective activities. The human transmembrane proteins,
XX polynucleotides encoding them and other compositions and methods from the
XX present invention, can be used for the diagnosis, treatment or prevention
XX of immune, reproductive, smooth muscle, neurological, gastrointestinal,
XX developmental and cell proliferative disorders. The HTMPN's can be used
XX to treat or prevent disorders associated with a decreased expression or
XX activity of HTMPN
XX
XX Sequence 129 AA;

Query Match      100.0%; Score 170; DB 3; Length 129;
Best Local Similarity 100.0%; Pred. No. 3.5e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARGSLRLLRLVLLGLWLLALLRSVAGEQAPGTAP 35
DB 1 MARGSLRLLRLVLLGLWLLALLRSVAGEQAPGTAP 35

RESULT 9
AAU03498
ID AAU03498 standard; protein; 129 AA.
XX
XX AAU03498;
XX
XX 26-SEP-2001 (first entry)
XX
XX Human TWEAK receptor (TWEAKR) polypeptide.
XX TWEAK receptor; TWEAKR; tumour necrosis factor; TNF; angiogenesis;
```

KW ocular neovascularisation; diabetic retinopathy; neovascular glaucoma;  
 KW retinoblastoma; retinopathy of prematurity; retrolental fibroplasia;  
 KW rubeosis; uveitis; macular degeneration; arthritis; rheumatism;  
 KW corneal graft neovascularisation; psoriasis; benign tumour; haemophilic joint;  
 KW malignant tumour; sarcoma; carcinoma; benign tumour; haemophilic joint;  
 KW preneoplastic condition; myocardial angiogenesis; wound granulation;  
 KW scleroderma; vascular adhesion; telangiectasia; ischaemia; human;  
 KW atherosclerotic plaque neovascularisation; coronary atherosclerosis;  
 KW peripheral atherosclerosis.

XX Homo sapiens.

OS  
 XX  
 XX  
 FH Key Location/Qualifiers  
 FT Domain 1..78  
 FT Peptide /note= "Extracellular domain"  
 FT Peptide 1..27  
 FT Protein /note= "Signal peptide"  
 FT Protein 28..129  
 FT Domain /note= "Mature human TWEAKR protein"  
 FT Domain 79..101  
 FT Domain /note= "Transmembrane domain"  
 FT Domain 102..129  
 FT Domain /note= "Intracellular domain"

XX WO200145730-A2.

XX 28-JUN-2001.

XX 19-DEC-2000; 2000WO-US034755.

XX 20-DEC-1999; 99US-0172878P.

XX 10-MAY-2000; 2000US-0203347P.

XX (IMV) IMMUNEX CORP.

XX Wiley SR;

XX WPI; 2001-417975/44.

XX N-PSDB; AAS03963.

XX Modulating angiogenesis in a mammal for treating diseases mediated by angiogenesis, e.g. solid tumors and vascular deficiencies of cardiac or peripheral tissue, by administering antagonist or agonist of TWEAK receptor.

XX Example 1; Fig 1; 46pp; English.

XX The sequence represents the human TWEAK receptor (TWEAKR) protein. The TWEAK protein is a member of the tumour necrosis factor (TNF) family and induces angiogenesis. TWEAKR may therefore be used to screen for and develop TWEAKR agonists and antagonists for the modulation of angiogenesis, to be used in the treatment and diagnosis of human disease. The disorders mediated by angiogenesis include ocular disorders characterised by ocular neovascularisation such as diabetic retinopathy, neovascular glaucoma, retinoblastoma, retinopathy of prematurity, retrolental fibroplasia, rubeosis, uveitis, macular degeneration and corneal graft neovascularisation, and inflammatory diseases such as arthritis, rheumatism and psoriasis. Other treatable diseases include malignant and metastatic conditions such as sarcomas and carcinomas, benign tumors and preneoplastic conditions, myocardial angiogenesis, haemophilic joints, scleroderma, vascular adhesions, atherosclerotic plaque neovascularisation, telangiectasia, wound granulation, coronary atherosclerosis, peripheral atherosclerosis and ischaemia

XX Sequence 129 AA;

Query Match 100.0%; Score 170; DB 4; Length 129;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-16;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARGSLRLLRLVGLWLLRLSVAGEQAPGTAP 35

Db 1 MARGSLRLLRLVGLWLLRLSVAGEQAPGTAP 35

RESULT 10

ABP61512

ID ABP61512 standard; protein; 129 AA.

XX ABP61512;

AC ABP61512;

XX 30-SEP-2002 (first entry)

XX Human NF-kB activating protein SEQ ID NO 178.

XX Human; NF-kB; nuclear factor kappa B; mouse; antiinflammatory;  
 KW immunomodulator; cytostatic; antiinfective; osteopathic; nootropic;  
 KW neuroprotective; anti-HIV; autoimmune disease; cancer; infection;  
 KW bone disease; AIDS; neurodegenerative disease; ischaemic disorder.

XX Homo sapiens.

XX WO200253737-A1.

XX 11-JUL-2002.

XX 25-DEC-2001; 2001WO-JP011389.

XX 28-DEC-2000; 2000JP-00402288.

XX 26-MAR-2001; 2001JP-00088912.

XX 24-AUG-2001; 2001JP-00254018.

XX (ASAH) ASAHI KASEI KOGYO KK.

XX Matsuda A, Honda G, Muramatsu S, Nagano Y;

XX WPI; 2002-583617/62.

XX N-PSDB; ABQ92000.

XX NF-approximatelykB activating gene and expressed protein, applicable in diagnosis and screening inhibitors or promoters to control excessive activation or inhibition for treating e.g. inflammations, autoimmune diseases and cancer.

XX Claim 4; Page 814-815; 841pp; Japanese.

XX The invention relates to a purified protein (I), comprising one of 90 fully defined sequences (ABP61424-ABP61513) or a protein based on any of the sequences but with some amino acids deleted, substituted or added and with a NF-kB (nuclear factor kappa B) activating effect. The protein and encoding gene (ABQ91912-ABQ92001) are useful in diagnosis and screening inhibitors or promoters to control excessive activation or inhibition and for treating e.g. inflammations, autoimmune diseases, cancers, infections, bone diseases, AIDS, neurodegenerative diseases or ischaemic disorders

XX Sequence 129 AA;

Query Match 100.0%; Score 170; DB 5; Length 129;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-16;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARGSLRLLRLVGLWLLRLSVAGEQAPGTAP 35

Db 1 MARGSLRLLRLVGLWLLRLSVAGEQAPGTAP 35

RESULT 11

AAU79827

ID AAU79827 standard; protein; 129 AA.

XX AAU79827;

XX 15-JUL-2002 (first entry)

XX Human type 1 transmembrane protein Fn14.

XX Type 1 transmembrane protein Fn14; human; cytostatic; cardiant;  
KW vulnary; TWEAK agonist; Fn14 agonist; angiogenesis; tumour progression;  
KW tumour necrosis factor family; TNF family; TWEAK receptor;  
KW myocardial ischaemic condition; myocardial infarction; wound healing;  
KW burn healing; gastric ulcer; tissue transplantation;  
KW organ transplantation; neovascularisation; vascular insufficiency;  
KW cancer; inflammatory macular degeneration; diabetic retinopathy.  
XX  
OS Homo sapiens.  
XX WO200222166-A2.  
PN  
XX  
PD 21-MAR-2002.  
XX  
XX  
PF 12-SEP-2001; 2001WO-US028451.  
XX  
XX  
PR 14-SEP-2000; 2000US-023355P.  
XX  
XX (BIOJ) BIOGEN INC.  
PA  
XX Browning J, Burky L, Jakubowski A, Zheng T;  
PI WPI; 2002-383103/41.  
XX  
XX Methods of modulating angiogenesis and inhibiting tumor progression,  
PT using TWEAK receptor agonists.  
PT  
XX Disclosure; Fig 10A; 37pp; English.  
XX  
XX The invention describes methods of modulating angiogenesis and inhibiting  
CC tumour progression using TWEAK (a novel member of the tumour necrosis  
CC factor or TNF family) receptor agonists. Conditions which can be treated  
CC using the agonists include myocardial ischaemic conditions (e.g.  
CC myocardial infarction), wound healing (e.g. burn healing and healing of  
CC gastric ulcers), and tissue and organ transplantations to promote  
CC neovascularisation, particularly in subjects suffering from vascular  
CC insufficiency (e.g. diabetic patients). Inhibition of angiogenesis and  
CC subsequently neovascularisation is useful in treatment of cancer,  
CC inflammatory macular degeneration and diabetic retinopathy. This sequence  
CC represents the human type 1 transmembrane protein Fn14, a TWEAK receptor  
CC described in the invention  
XX  
SQ Sequence 129 AA;  
Query Match 100.0%; Score 170; DB 5; Length 129;  
Best Local Similarity 100.0%; Pred. No. 3.5e-16;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MARGSLRRLRLVLLGLWLLALLRSVAGEQAPGTAP 35  
DB 1 MARGSLRRLRLVLLGLWLLALLRSVAGEQAPGTAP 35  
RESULT 12  
ADA56889  
ID ADA56889 standard; protein; 129 AA.  
XX  
AC ADA56889;  
XX  
XX 20-NOV-2003 (first entry)  
DT  
XX Human secreted protein #172.  
DE  
XX immunosuppressive; antiinflammatory; antiasthmatic; antiallergic;  
KW cytostatic; cerebroprotective; neuroprotective; nootropic;  
KW cardiovascular; antiarteriosclerotic; gene therapy;  
KW human secreted protein; immune disorder; inflammation;  
KW respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;  
KW inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;  
KW multiple sclerosis; ischaemic brain injury; Parkinson's disease;  
KW Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;  
KW triple helix formation; antisense gene therapy; forensic biology.

XX Homo sapiens.  
OS  
XX WO2002102994-A2.  
PN  
XX 27-DEC-2002.  
PD  
XX 19-MAR-2002; 2002WO-US008278.  
PF  
XX 21-MAR-2001; 2001US-0277340P.  
PR 19-JUL-2001; 2001US-0306171P.  
XX 13-NOV-2001; 2001US-0331287P.  
XX (HUMA-) HUMAN GENOME SCI INC.  
PA  
XX Rosen CA, Ruben SM;  
PI WPI; 2003-167512/16.  
XX N-PSDB; ADA55993.  
DR  
XX New human secreted polypeptides and polynucleotides, useful for  
PT diagnosing, treating or preventing e.g. immune disorders, inflammatory  
PT conditions, respiratory disorders, cancers, CNS disorders, or  
PT neurodegenerative disorders.  
XX  
XX Claim 13; SEQ ID NO 1079; 1754pp; English.  
PS  
XX The invention relates to 592 new human secreted polypeptides useful for  
CC diagnosing, treating or preventing e.g. immune disorders, inflammatory  
CC conditions, respiratory disorders, cancers, CNS disorders, or  
CC neurodegenerative disorders, or polypeptides comprising an amino acid  
CC sequence at least 95% identical to the new sequences. The polypeptides,  
CC antibodies or antibody fragments that bind to the polypeptides, nucleic  
CC acids encoding the polypeptides, agonists or antagonists that binds to  
CC the polypeptide, are useful in preparing diagnostic or pharmaceutical  
CC compositions for diagnosing, treating or preventing an e.g. immune  
CC disorders, inflammatory conditions (e.g. inflammatory bowel disease,  
CC nephritis or Crohn's disease), respiratory disorders (e.g. asthma and  
CC allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders  
CC (e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative  
CC disorders (e.g. Parkinson's disease or Alzheimer's disease), and  
CC cardiovascular disorders (e.g. atherosclerosis or myocarditis). The  
CC polynucleotides are useful for chromosome identification, chromosome  
CC mapping, for controlling gene expression through triple helix formation  
CC or antisense DNA or RNA, in gene therapy, for identifying individuals  
CC from minute biological samples, in forensic biology, and as hybridization  
CC probes. The polypeptides are useful for as molecular weight markers on  
CC sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE)  
CC gels, to raise antibodies, for testing biological activities, and for  
CC treating or preventing neural disorders, immune system disorders,  
CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,  
CC renal, proliferative and/or cancerous diseases. This sequence corresponds  
CC to one of the polypeptide of the invention. Note: The sequence data for  
CC this patent did form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
XX Sequence 129 AA;  
Query Match 100.0%; Score 170; DB 6; Length 129;  
Best Local Similarity 100.0%; Pred. No. 3.5e-16;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MARGSLRRLRLVLLGLWLLALLRSVAGEQAPGTAP 35  
DB 1 MARGSLRRLRLVLLGLWLLALLRSVAGEQAPGTAP 35  
RESULT 13  
ABU56716  
ID ABU56716 standard; protein; 129 AA.  
XX  
AC ABU56716;

XX 02-APR-2003 (first entry)  
XX Lung cancer-associated polypeptide #309.  
XX Lung cancer-associated polypeptide; cytostatic; emphysema;  
XX antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;  
KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;  
KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;  
KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.  
XX Unidentified.  
OS WO200286443-A2.  
PN 31-OCT-2002.  
XX 18-APR-2002; 2002WO-US012476.  
XX 18-APR-2001; 2001US-0284770P.  
PR 10-MAY-2001; 2001US-0290492P.  
PR 09-NOV-2001; 2001US-0339245P.  
PR 13-NOV-2001; 2001US-0350666P.  
PR 29-NOV-2001; 2001US-0334370P.  
PR 12-APR-2002; 2002US-0372246P.  
XX (EOSB-) EOS BIOTECHNOLOGY INC.  
XX Aziz N, Murray R;  
PI WPI; 2003-093161/08.  
XX N-PSDB; ABX76445.  
DR Detecting a lung cancer-associated transcript in a cell from a patient  
XX for treating lung cancer, by contacting a biological sample from the  
PT patient with a polynucleotide that exhibits increased or decreased  
PT expression in lung cancer.  
XX Claim 27; Page 429; 453pp; English.  
XX The invention relates to a method for detecting a lung cancer-associated  
CC transcript in a cell from a patient, comprising contacting a biological  
CC sample from the patient with a polynucleotide that selectively hybridises  
CC to a sequence that is at least 80 % identical to a gene that exhibits  
CC increased or decreased expression in lung cancer samples. Lung cancer-  
CC associated polynucleotides and polypeptides are used for identifying a  
CC compound that modulates a lung cancer-associated polypeptide, for  
CC inhibiting proliferation of a lung cancer-associated cell to treat lung  
CC cancer in a patient and for treating a mammal having lung cancer by  
CC administering a modulatory compound identified. The methods are useful  
CC for treating lung cancer, such as small cell lung cancer, non-small cell  
CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,  
CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,  
CC hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and  
CC bronchiectasis. The genes, polynucleotides and polypeptides are useful  
CC for diagnostic purposes and as targets for screening for therapeutic  
CC compounds that modulate lung cancer, such as antibodies. Sequences  
CC ABU56408-ABU56745 represent lung cancer-associated polypeptides of the  
CC invention  
XX  
SQ Sequence 129 AA;  
Query Match 100.0%; Score 170; DB 6; Length 129;  
Best Local Similarity 100.0%; Pred. No. 3.5e-16;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAP 35  
RESULT 14  
ADC74112

AD74112 standard; protein; 129 AA.  
ADC74112;  
01-JAN-2004 (first entry)  
Human secreted protein - SEQ ID 745.  
antianemic; antirheumatic; antiarthritic; antiinflammatory; antithyroid;  
antidiabetic; immunosuppressive; dermatologic; nephrotropic;  
antiparkinsonian; neuroprotective; nootropic; antibacterial; virucide;  
fungicide; antiparasitic; antiarteriosclerotic; vulnerary; cytostatic;  
haemopoietic; haematologic; anaemia; autoimmune disorder;  
rheumatoid arthritis; inflammation; Grave's disease; diabetes;  
systemic lupus erythematosus; glomerulonephritis; neurodegenerative;  
Parkinson's; Alzheimer's; wound; hyperproliferative; atherosclerosis;  
cancer; bacterial; viral; fungal; parasitic infection; gene therapy;  
human.  
Homo sapiens.  
WO2003038063-A2.  
08-MAY-2003.  
19-MAR-2002; 2002WO-US008277.  
21-MAR-2001; 2001US-0277340P.  
19-JUL-2001; 2001US-0306171P.  
13-NOV-2001; 2001US-0331287P.  
(HUMA-) HUMAN GENOME SCI INC.  
Rosen CA, Ruben SM;  
WPI; 2003-430516/40.  
N-PSDB; ADC73497.  
New human secreted polypeptide for diagnosing, preventing or treating  
hematopoietic or hematologic disorders (e.g. anemia), autoimmune  
disorders (e.g. diabetes) or hyperproliferative disorders (e.g. cancer or  
atherosclerosis).  
Claim 16; SEQ ID NO 745; 2272pp; English.  
The invention relates to a novel human secreted polypeptide comprising a  
defined sequence given in the specification. The polypeptide, nucleic  
acid molecule, antibody, agonist or antagonist of the invention may be  
useful for preparing a composition for diagnosing or treating a  
haemopoietic or haematologic disorder such as anaemia, autoimmune  
disorders such as rheumatoid arthritis, inflammation, Grave's disease,  
diabetes, systemic lupus erythematosus or glomerulonephritis, and  
neurodegenerative disorders including Parkinson's disease and Alzheimer's  
disease, wounds and hyperproliferative disorders including  
atherosclerosis or cancer, as well as bacterial, viral, fungal or  
parasitic infections. The polypeptide may also be used during gene  
therapy procedures and for identifying a binding partner by contacting  
the polypeptide with a binding partner and determining whether the  
binding partner increases or decreases the activity of the polypeptide.  
The current sequence is that of the human secreted protein of the  
invention.  
SQ Sequence 129 AA;  
Query Match 100.0%; Score 170; DB 7; Length 129;  
Best Local Similarity 100.0%; Pred. No. 3.5e-16;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAP 35  
Db 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAP 35

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RESULT 15
ADD37867
ID ADD37867 standard; protein; 129 AA.
XX
AC ADD37867;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human secreted protein #50.
XX
KW human secreted protein; Antiallergic; Antiinflammatory; Antibacterial;
XX Anti-HIV; Cytostatic; Immunosuppressive; Hemostatic.
XX
OS Homo sapiens.
XX
PN WO200290526-A2.
XX
PD 14-NOV-2002.
XX
PF 19-MAR-2002; 2002WO-US008279.
XX
PR 21-MAR-2001; 2001US-0277340P.
XX
PR 19-JUL-2001; 2001US-0306171P.
XX
PR 13-NOV-2001; 2001US-0331287P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
WPI; 2003-140218/13.
XX
New human secreted proteins and nucleic acid molecules, useful for
preparing a diagnostic or pharmaceutical composition for diagnosing or
treating allergic or asthmatic disorders, or related immediate
hypersensitivity disorders.
XX
PS Claim 1; SEQ ID NO 349; 1323pp; English.
XX
The present invention relates to an isolated polypeptide or human
secreted protein. The polypeptides, nucleic acid molecules, antibodies or
their fragments, and agonists or antagonists that bind are useful for
preparing a diagnostic or pharmaceutical composition for diagnosing or
treating allergic or asthmatic disorders. The polypeptide is also useful
for identifying a binding partner by contacting the polypeptide with a
binding partner, and determining whether the binding partner increases or
decreases the activity of the polypeptide. The polypeptides and nucleic
acid molecules are also useful for detecting, preventing, diagnosing,
prognosticating, treating or ameliorating inflammatory disorders
neoplastic diseases, wound healing and disorders of epithelial cell
proliferation, immune disorders, cardiovascular disorders, blood-related
disorders, infectious diseases, endocrine disorders, or gastrointestinal
disorders. The nucleic acids are also useful for chromosome
identification, radiation hybrid mapping or long-range restriction
mapping, as molecular weight markers, or as hybridization or diagnostic
probes. The polypeptides and antibodies are useful for providing
immunological probes for differential identification of the tissues
immunohistochemistry assays. The present sequence represents a human
secreted protein.
XX
SQ Sequence 129 AA;
Query Match 100.0%; Score 170; DB 7; Length 129;
Best Local Similarity 100.0%; Pred. No. 3.5e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MARGSLRLRLRLVGLWALLRSVAGEQPGTAP 35
Db 1 MARGSLRLRLRLVGLWALLRSVAGEQPGTAP 35
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Job time : 57.5702 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 10, 2005, 18:17:36 ; Search time 40.6798 Seconds  
(without alignments)  
281.128 Million cell updates/sec

Title: US-10-062-831-59\_COPY\_1\_35

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1376875 seqs, 326749119 residues

Total number of hits satisfying chosen parameters: 1376875

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

#### Database :

Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US05\_NEW\_PUB.pep.\*
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- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
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- 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	170	100.0	112	15 US-10-351-334-139	Sequence 139, App
2	170	100.0	114	14 US-10-062-831-59	Sequence 59, Appl
3	170	100.0	114	14 US-10-062-599-59	Sequence 59, Appl
4	170	100.0	129	9 US-09-742-454A-4	Sequence 4, Appl
5	170	100.0	129	9 US-09-883-777-5	Sequence 4, Appl
6	170	100.0	129	14 US-10-024-298A-178	Sequence 178, App
7	170	100.0	129	14 US-10-042-211A-178	Sequence 178, App
8	170	100.0	129	15 US-10-331-496A-37	Sequence 37, Appl
9	170	100.0	129	15 US-10-295-027-444	Sequence 444, App
10	170	100.0	129	15 US-10-295-027-1305	Sequence 1305, App
11	170	100.0	129	15 US-10-617-217A-178	Sequence 178, App
12	170	100.0	155	15 US-10-351-334-284	Sequence 284, App
13	170	100.0	156	15 US-10-351-334-228	Sequence 228, App

14	170	100.0	300	9 US-09-883-777-9	Sequence 9, Appl
15	170	100.0	309	9 US-09-742-454A-7	Sequence 7, Appl
16	170	100.0	309	9 US-09-883-777-7	Sequence 7, Appl
17	97	57.1	129	9 US-09-742-454A-5	Sequence 5, Appl
18	97	57.1	129	9 US-09-883-777-5	Sequence 5, Appl
19	58	34.1	577	16 US-10-437-963-182042	Sequence 182042, A
20	56.5	33.2	671	15 US-10-282-122A-59634	Sequence 59634, A
21	55	32.4	465	14 US-10-156-761-13252	Sequence 13252, A
22	54.5	32.1	1120	15 US-10-262-839-6	Sequence 6, Appl
23	54.5	32.1	1188	15 US-10-291-265-338	Sequence 338, App
24	54.5	32.1	1188	15 US-10-291-265-810	Sequence 810, App
25	54.5	32.1	1189	10 US-09-984-130-35	Sequence 35, Appl
26	54.5	32.1	1189	10 US-09-836-353A-35	Sequence 35, Appl
27	54.5	32.1	1189	15 US-10-262-839-4	Sequence 4, Appl
28	54	31.8	77	9 US-09-764-860-332	Sequence 332, App
29	54	31.8	77	14 US-10-074-095-332	Sequence 332, App
30	54	31.8	77	15 US-10-212-872-332	Sequence 332, App
31	54	31.8	300	9 US-09-953-499-10	Sequence 10, Appl
32	54	31.8	300	14 US-10-265-542-10	Sequence 10, Appl
33	54	31.8	300	16 US-10-633-008-10	Sequence 10, Appl
34	54	31.8	300	16 US-10-785-220-10	Sequence 10, Appl
35	54	31.8	300	16 US-10-785-221-10	Sequence 10, Appl
36	54	31.8	300	16 US-10-785-433-10	Sequence 10, Appl
37	54	31.8	319	10 US-09-847-102A-61	Sequence 61, Appl
38	54	31.8	404	14 US-10-156-761-13020	Sequence 13020, A
39	54	31.8	647	10 US-09-847-102A-44	Sequence 44, Appl
40	54	31.8	647	14 US-10-285-976-39	Sequence 39, Appl
41	53.5	31.5	144	15 US-10-425-114-38365	Sequence 38365, A
42	53.5	31.5	159	15 US-10-425-114-48240	Sequence 48240, A
43	53.5	31.5	2098	14 US-10-132-134-36	Sequence 36, Appl
44	53	31.2	692	14 US-10-156-761-13135	Sequence 13135, A
45	53	31.2	1102	15 US-10-282-122A-67640	Sequence 67640, A

#### ALIGNMENTS

#### RESULT 1

US-10-351-334-139  
; Sequence 139, Application US/10351334  
; Publication No. US20040034196A1  
; GENERAL INFORMATION:  
; APPLICANT: Komatsoulis et al  
; TITLE OF INVENTION: 98 Human Secreted Proteins  
; FILE REFERENCE: P2031P2  
; CURRENT APPLICATION NUMBER: US/10/351,334  
; PRIOR FILING DATE: 2003-01-27  
; PRIOR APPLICATION NUMBER: 60/350,898  
; PRIOR FILING DATE: 2002-01-25  
; PRIOR APPLICATION NUMBER: 09/489,847  
; PRIOR FILING DATE: 2000-01-24  
; PRIOR APPLICATION NUMBER: PCT/US99/17130  
; PRIOR FILING DATE: 1999-07-29  
; PRIOR APPLICATION NUMBER: 60/094,657  
; PRIOR FILING DATE: 1998-07-30  
; PRIOR APPLICATION NUMBER: 60/095,486  
; PRIOR FILING DATE: 1998-08-05  
; PRIOR APPLICATION NUMBER: 60/096,319  
; PRIOR FILING DATE: 1998-08-12  
; PRIOR APPLICATION NUMBER: 60/095,454  
; PRIOR FILING DATE: 1998-08-06  
; PRIOR APPLICATION NUMBER: 60/095,455  
; NUMBER OF SEQ ID NOS: 376  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 139  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-10-351-334-139

Query Match 100.0%; Score 170; DB 15; Length 112;  
Best Local Similarity 100.0%; Pred. No. 2.3e-14;

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Qy 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAP 35
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Db 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAP 35

RESULT 2
US-10-062-831-59
; Sequence 59, Application US/10062831
; Publication No. US20030105297A1
; GENERAL INFORMATION:
; APPLICANT: Steven M. Ruben, et al.
; TITLE OF INVENTION: 32 Human Secreted Proteins
; FILE REFERENCE: PZ006P1
; CURRENT APPLICATION NUMBER: US/10/062,831
; PRIOR FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: 09/690,454
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: PCT/US98/10868
; PRIOR FILING DATE: May 28, 1998
; PRIOR APPLICATION NUMBER: 60/044,039
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,093
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,190
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/050,935
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,101
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,356
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/056,250
; PRIOR FILING DATE: August 29, 1997
; PRIOR APPLICATION NUMBER: 60/056,296
; PRIOR FILING DATE: August 29, 1997
; PRIOR APPLICATION NUMBER: 60/056,293
; PRIOR FILING DATE: August 29, 1997
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 59
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (114)
; OTHER INFORMATION: Xaa equals stop translation
US-10-062-831-59

Query Match 100.0%; Score 170; DB 14; Length 114;
Best Local Similarity 100.0%; Pred. No. 2.3e-14;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAP 35

RESULT 4
US-09-742-454A-4
; Sequence 4, Application US/09742454A
; Patent No. US20020041876A1
; GENERAL INFORMATION:
; APPLICANT: WILEY, Steven R.
; TITLE OF INVENTION: TWEAK Receptor
; FILE REFERENCE: 2968-B
; CURRENT APPLICATION NUMBER: US/09/742,454A
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: 60/203,347
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-742-454A-4

Query Match 100.0%; Score 170; DB 9; Length 129;
Best Local Similarity 100.0%; Pred. No. 2.6e-14;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5
US-09-883-777-4
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; Sequence 4, Application US/09883777  
; Patent No. US20020110853A1  
; GENERAL INFORMATION:  
; APPLICANT: Wiley, Steven R.  
; FILE REFERENCE: 2968-C  
; TITLE OF INVENTION: TWEAK RECEPTOR  
; CURRENT APPLICATION NUMBER: US/09/883,777  
; PRIOR FILING DATE: 2001-06-18  
; PRIOR APPLICATION NUMBER: US 60/172,878  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: US 60/203,347  
; PRIOR FILING DATE: 2000-05-10  
; PRIOR APPLICATION NUMBER: PCT/US00/34755  
; PRIOR FILING DATE: 2000-12-19  
; PRIOR APPLICATION NUMBER: US 09/742,454  
; PRIOR FILING DATE: 2000-12-19  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 129  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-09-883-777-4

Query Match 100.0%; Score 170; DB 9; Length 129;  
Best Local Similarity 100.0%; Pred. No. 2.6e-14;  
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QY 1 MARGSLRLLRLVLGLWLALLRSVAGEQAPGTAP 35  
|||||  
DB 1 MARGSLRLLRLVLGLWLALLRSVAGEQAPGTAP 35

RESULT 6  
US-10-024-298A-178  
; Sequence 178, Application US/10024298A  
; Publication No. US20030143540A1  
; GENERAL INFORMATION:  
; APPLICANT: ASAHU KASEI KABUSHIKI KAISHA  
; APPLICANT: Akio MATSUDA  
; APPLICANT: Goichi HONDA  
; APPLICANT: Shuji MORAWATSU  
; APPLICANT: Yukiko NAGANO  
; TITLE OF INVENTION: NF-K B Activating Gene  
; FILE REFERENCE: 1254-0191P  
; CURRENT APPLICATION NUMBER: US/10/024,298A  
; CURRENT FILING DATE: 2003-04-08  
; PRIOR APPLICATION NUMBER: 60/314,385  
; PRIOR FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: 60/278,641  
; PRIOR FILING DATE: 2001-03-26  
; PRIOR APPLICATION NUMBER: 60/258,315  
; PRIOR FILING DATE: 2000-12-28  
; PRIOR APPLICATION NUMBER: JP254018/2001  
; PRIOR FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: JP0088912/2001  
; PRIOR FILING DATE: 2001-03-26  
; PRIOR APPLICATION NUMBER: JP402288/2000  
; PRIOR FILING DATE: 2000-12-28  
; NUMBER OF SEQ ID NOS: 182  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 178  
; LENGTH: 129  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-024-298A-178

Query Match 100.0%; Score 170; DB 14; Length 129;  
Best Local Similarity 100.0%; Pred. No. 2.6e-14;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARGSLRLLRLVLGLWLALLRSVAGEQAPGTAP 35  
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Db 1 MARGSLRLLRLVLGLWLALLRSVAGEQAPGTAP 35

## RESULT 7

US-10-042-211A-178  
; Sequence 178, Application US/10042211A  
; Publication No. US20030170719A1  
; GENERAL INFORMATION:  
; APPLICANT: MATSUDA, Akio et al.  
; TITLE OF INVENTION: NFkB Activating Gene  
; FILE REFERENCE: 1254-0192P  
; CURRENT APPLICATION NUMBER: US/10/042,211A  
; CURRENT FILING DATE: 2002-01-11  
; PRIOR APPLICATION NUMBER: JP 2000-402288  
; PRIOR FILING DATE: 2000-12-28  
; PRIOR APPLICATION NUMBER: JP 2001-088912  
; PRIOR FILING DATE: 2001-03-26  
; PRIOR APPLICATION NUMBER: JP 2001-254018  
; PRIOR FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: US 60/258,315  
; PRIOR FILING DATE: 2000-12-28  
; PRIOR APPLICATION NUMBER: US 60/278,640  
; PRIOR FILING DATE: 2001-03-26  
; PRIOR APPLICATION NUMBER: US 60/314,385  
; PRIOR FILING DATE: 2001-08-24  
; NUMBER OF SEQ ID NOS: 182  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 178  
; LENGTH: 129  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-042-211A-178

Query Match 100.0%; Score 170; DB 14; Length 129;  
Best Local Similarity 100.0%; Pred. No. 2.6e-14;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARGSLRLLRLVLGLWLALLRSVAGEQAPGTAP 35  
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DB 1 MARGSLRLLRLVLGLWLALLRSVAGEQAPGTAP 35

## RESULT 8

US-10-331-496A-37  
; Sequence 37, Application US/10331496A  
; Publication No. US20030228305A1  
; GENERAL INFORMATION:  
; APPLICANT: FRANTZ, GRETCHEN  
; APPLICANT: HILLAN, KENNETH J.  
; APPLICANT: PHILLIPS, HEIDI S.  
; APPLICANT: POLAKIS, PAUL  
; APPLICANT: SMITH, VICTORIA  
; APPLICANT: SPENCER, SUSAN D.  
; APPLICANT: WILLIAMS, P. MICKEY  
; APPLICANT: WU, THOMAS D.  
; APPLICANT: ZHANG, ZEMIN  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND  
; FILE REFERENCE: P5014R1-PCT  
; CURRENT APPLICATION NUMBER: US/10/331,496A  
; CURRENT FILING DATE: 2002-12-30  
; PRIOR APPLICATION NUMBER: US 60/345,444  
; PRIOR FILING DATE: 2002-01-02  
; PRIOR APPLICATION NUMBER: US 60/351,885  
; PRIOR FILING DATE: 2002-01-25  
; PRIOR APPLICATION NUMBER: US 60/360,066  
; PRIOR FILING DATE: 2002-02-25  
; PRIOR APPLICATION NUMBER: US 60/362,004  
; PRIOR FILING DATE: 2002-03-05  
; PRIOR APPLICATION NUMBER: US 60/366,869  
; PRIOR FILING DATE: 2002-03-20  
; PRIOR APPLICATION NUMBER: US 60/366,284  
; PRIOR FILING DATE: 2002-03-21

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RESULT 11
US-10-617-217A-178
; Sequence 178, Application US/10617217A
; Publication No. US20040081986A1
; GENERAL INFORMATION:
; APPLICANT: MATSUDA, Akio et al.
; TITLE OF INVENTION: NF-KB ACTIVATING GENE
; FILE REFERENCE: 1254-0229P

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;; CURRENT APPLICATION NUMBER: US/10/617,217A  
;; CURRENT FILING DATE: 2003-07-11  
;; PRIOR APPLICATION NUMBER: JP 2000-402288  
;; PRIOR FILING DATE: 2000-12-28  
;; PRIOR APPLICATION NUMBER: JP 2001-088912  
;; PRIOR FILING DATE: 2001-03-26  
;; PRIOR APPLICATION NUMBER: JP 2001-254018  
;; PRIOR FILING DATE: 2001-08-24  
;; PRIOR APPLICATION NUMBER: US 60/258,315  
;; PRIOR FILING DATE: 2000-12-28  
;; PRIOR APPLICATION NUMBER: US 60/278,640  
;; PRIOR FILING DATE: 2001-03-26  
;; PRIOR APPLICATION NUMBER: US 60/314,385  
;; PRIOR FILING DATE: 2001-08-24  
;; NUMBER OF SEQ ID NOS: 224  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 178  
;; LENGTH: 129  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-617-217A-178

Query Match 100.0%; Score 170; DB 15; Length 129;  
Best Local Similarity 100.0%; Pred. No. 2.6e-14;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARGSLRLLRLVLLGLWLLALLRSVAGEQAPGTAP 35  
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Db 1 MARGSLRLLRLVLLGLWLLALLRSVAGEQAPGTAP 35

RESULT 12  
US-10-351-334-284  
;; Sequence 284, Application US/10351334  
;; Publication No. US20040034196A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Komatsoulis et al  
;; TITLE OF INVENTION: 98 Human Secreted Proteins  
;; CURRENT APPLICATION NUMBER: US/10/351,334  
;; CURRENT FILING DATE: 2003-01-27  
;; PRIOR APPLICATION NUMBER: 60/350,898  
;; PRIOR FILING DATE: 2002-01-25  
;; PRIOR APPLICATION NUMBER: 09/489,847  
;; PRIOR FILING DATE: 2000-01-24  
;; PRIOR APPLICATION NUMBER: PCT/US99/17130  
;; PRIOR FILING DATE: 1999-07-29  
;; PRIOR APPLICATION NUMBER: 60/094,657  
;; PRIOR FILING DATE: 1998-07-30  
;; PRIOR APPLICATION NUMBER: 60/095,486  
;; PRIOR FILING DATE: 1998-08-05  
;; PRIOR APPLICATION NUMBER: 60/096,319  
;; PRIOR FILING DATE: 1998-08-12  
;; PRIOR APPLICATION NUMBER: 60/095,454  
;; PRIOR FILING DATE: 1998-08-06  
;; PRIOR APPLICATION NUMBER: 60/095,455  
;; PRIOR FILING DATE: 1998-08-06  
;; NUMBER OF SEQ ID NOS: 376  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 284  
;; LENGTH: 155  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-351-334-284

Query Match 100.0%; Score 170; DB 15; Length 155;  
Best Local Similarity 100.0%; Pred. No. 3.2e-14;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARGSLRLLRLVLLGLWLLALLRSVAGEQAPGTAP 35  
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Db 1 MARGSLRLLRLVLLGLWLLALLRSVAGEQAPGTAP 35

RESULT 13  
US-10-351-334-228  
;; Sequence 228, Application US/10351334  
;; Publication No. US20040034196A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Komatsoulis et al  
;; TITLE OF INVENTION: 98 Human Secreted Proteins  
;; CURRENT APPLICATION NUMBER: US/10/351,334  
;; CURRENT FILING DATE: 2003-01-27  
;; PRIOR APPLICATION NUMBER: 60/350,898  
;; PRIOR FILING DATE: 2002-01-25  
;; PRIOR APPLICATION NUMBER: 09/489,847  
;; PRIOR FILING DATE: 2000-01-24  
;; PRIOR APPLICATION NUMBER: PCT/US99/17130  
;; PRIOR FILING DATE: 1999-07-29  
;; PRIOR APPLICATION NUMBER: 60/094,657  
;; PRIOR FILING DATE: 1998-07-30  
;; PRIOR APPLICATION NUMBER: 60/095,486  
;; PRIOR FILING DATE: 1998-08-05  
;; PRIOR APPLICATION NUMBER: 60/096,319  
;; PRIOR FILING DATE: 1998-08-12  
;; PRIOR APPLICATION NUMBER: 60/095,454  
;; PRIOR FILING DATE: 1998-08-06  
;; PRIOR APPLICATION NUMBER: 60/095,455  
;; PRIOR FILING DATE: 1998-08-06  
;; NUMBER OF SEQ ID NOS: 376  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 228  
;; LENGTH: 156  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
;; NAME/KEY: SITE  
;; LOCATION: (156)  
;; OTHER INFORMATION: Xaa equals stop translation  
US-10-351-334-228

Query Match 100.0%; Score 170; DB 15; Length 156;  
Best Local Similarity 100.0%; Pred. No. 3.2e-14;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARGSLRLLRLVLLGLWLLALLRSVAGEQAPGTAP 35  
|||||  
Db 1 MARGSLRLLRLVLLGLWLLALLRSVAGEQAPGTAP 35

RESULT 14  
US-09-883-777-9  
;; Sequence 9, Application US/09883777  
;; Patent No. US20020110853A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Wiley, Steven R.  
;; TITLE OF INVENTION: TWEAK RECEPTOR  
;; FILE REFERENCE: 2968-C  
;; CURRENT APPLICATION NUMBER: US/09/883,777  
;; CURRENT FILING DATE: 2001-06-18  
;; PRIOR APPLICATION NUMBER: US 60/172,878  
;; PRIOR FILING DATE: 1999-12-20  
;; PRIOR APPLICATION NUMBER: US 60/203,347  
;; PRIOR FILING DATE: 2000-05-10  
;; PRIOR APPLICATION NUMBER: PCT/US00/34755  
;; PRIOR FILING DATE: 2000-12-19  
;; PRIOR APPLICATION NUMBER: US 09/742,454  
;; PRIOR FILING DATE: 2000-12-19  
;; NUMBER OF SEQ ID NOS: 16  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 9  
;; LENGTH: 300  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:

Mon Feb 14 07:22:42 2005

OTHER INFORMATION: Human TWEAK receptor fusion protein construct  
US-09-883-777-9

Query Match	100.0%;	Score 170;	DB 9;	Length 300;
Best Local Similarity	100.0%;	Pred. No. 6.1e-14;		
Matches 35:	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy 1 MARGSLRRLRLVLGLWLLALLRSVAGEQAPGTAP 35  
|||||

nb 1 MARGSLRRLRLVLGLWLLALLRSVAGEQAPGTAP 35  
|||||

RESULT 15

US-09-742-454A-7  
; Sequence 7, Application US/09742454A  
; Patent No. US20020041876A1

FILE NO. US2002001  
GENERAL INFORMATION:

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, GENERAL INFORMATION.
, APPLICANT: WILEY, Steven R.
, TITLE OF INVENTION: TWEAK Receptor
, FILE REFERENCE: 2968-B
, CURRENT APPLICATION NUMBER: US/08/742,454A
, CURRENT FILING DATE: 2000-12-19
, PRIOR APPLICATION NUMBER: 60/172,878
, PRIOR FILING DATE: 1999-12-20
, PRIOR APPLICATION NUMBER: 60/203,347
, PRIOR FILING DATE: 2000-05-10
, NUMBER OF SEQ ID NOS: 7
, SOFTWARE: PatentIn Ver. 2.0
, SEQ ID NO 7

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SEQ ID NO: 309  
LENGTH: 309

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; LENGTH: 305
; TYPE: PRT
; ORGANISM: Artificial Sequence

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; ORGANISM: Mus musculus
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; FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: human TWEAK
;   OTHER INFORMATION: receptor fusion protein construct
;   OTHER INFORMATION:
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; US-09-742-454A-7

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U.S.-09-742-454A-7

Query Match	100.0%;	Score 170;	DB 9;	Length 309;
Best Local Similarity	100.0%;	Pred. No. 6.3e-14;		
Matches 35:	Conservative	0;	Mismatches	0;
	Indels	0;	Gaps	0;

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1 MARGSLRRLLRLVLGLWLALLRSVAGEQAPGTAP 35 Db

Search completed: February 10, 2005, 18:43:36  
Job time : 41.6798 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2005, 18:02:18 ; Search time 14.4298 Seconds  
(without alignments)  
181.064 Million cell updates/sec

Title: US-10-062-831-59\_COPY\_1\_35

Perfect score: 170

Sequence: 1 MARGSLRRLRLVGLWLLRLSRVAGEQAPGTAP 35

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*

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2: /cgn2\_6/ptodata/1/iaa/5B.COMB.pap.\*  
3: /cgn2\_6/ptodata/1/iaa/6A.COMB.pap.\*  
4: /cgn2\_6/ptodata/1/iaa/6B.COMB.pap.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS.COMB.pap.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	170	100.0	112	4	US-09-489-847-139
2	170	100.0	114	4	US-09-690-454-59
3	170	100.0	129	4	US-09-883-777-4
4	170	100.0	129	4	US-09-949-016-6914
5	170	100.0	129	4	US-09-742-454A-4
6	170	100.0	155	4	US-09-489-847-284
7	170	100.0	156	4	US-09-489-847-228
8	170	100.0	300	4	US-09-883-777-9
9	170	100.0	309	4	US-09-883-777-7
10	170	100.0	309	4	US-09-742-454A-7
11	97	57.1	129	4	US-09-883-777-5
12	97	57.1	129	4	US-09-742-454A-5
13	54.5	32.1	1217	4	US-09-949-016-7892
14	54	31.8	300	4	US-09-254-465A-10
15	54	31.8	300	4	US-09-397-243D-12
16	54	31.8	300	4	US-09-953-499-10
17	53	31.2	38	4	US-09-471-276-1405
18	53	31.2	48	3	US-09-453-322B-14
19	52.5	30.9	680	4	US-09-489-039A-8422
20	52	30.6	108	4	US-09-513-999C-4205
21	52	30.6	518	4	US-09-893-737-84
22	52	30.6	598	4	US-09-252-991A-28599
23	52	30.6	957	4	US-09-949-016-6154
24	52	30.6	964	4	US-09-949-016-7431
25	51.5	30.3	422	4	US-09-902-540-11389
26	51	30.0	148	4	US-09-489-039A-11733
27	50.5	29.7	156	4	US-09-902-540-12764

28	50.5	29.7	432	3	US-08-702-665A-3	Sequence 3, Appli
29	50.5	29.7	441	3	US-09-151-102-4	Sequence 4, Appli
30	50.5	29.7	441	3	US-08-929-846-4	Sequence 4, Appli
31	50.5	29.7	441	4	US-08-663-584-4	Sequence 4, Appli
32	50	29.4	240	4	US-09-949-016-9266	Sequence 9266, Ap
33	50	29.4	386	3	US-09-321-961-5	Sequence 5, Appli
34	50	29.4	386	4	US-09-739-861A-5	Sequence 5, Appli
35	50	29.4	386	4	US-09-795-583-5	Sequence 5, Appli
36	49	28.8	427	4	US-09-550-645-2	Sequence 2, Appli
37	49	28.8	428	4	US-09-922-364A-32	Sequence 32, Appli
38	49	28.8	428	4	US-09-254-590-32	Sequence 32, Appli
39	49	28.8	428	4	US-10-115-415-32	Sequence 32, Appli
40	49	28.8	428	4	US-10-116-260-32	Sequence 32, Appli
41	49	28.8	428	4	US-10-115-671-32	Sequence 32, Appli
42	49	28.8	510	4	US-09-949-016-10021	Sequence 10021, A
43	49	28.8	1238	3	US-09-214-278-5	Sequence 5, Appli
44	49	28.8	1238	4	US-09-855-722-5	Sequence 5, Appli
45	49	28.8	1399	3	US-08-462-467B-14	Sequence 14, Appli

#### ALIGNMENTS

RESULT 1  
US-09-489-847-139  
; Sequence 139, Application US/09489847  
; Patent No. 6476195  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al  
; TITLE OF INVENTION: 98 Human Secreted Proteins  
; FILE REFERENCE: P2031P1  
; CURRENT APPLICATION NUMBER: US/09/489,847  
; CURRENT FILING DATE: 2000-01-24  
; EARLIER APPLICATION NUMBER: PCT/US99/17130  
; EARLIER FILING DATE: 1999-07-29  
; EARLIER APPLICATION NUMBER: 60/094,657  
; EARLIER FILING DATE: 1998-07-30  
; EARLIER APPLICATION NUMBER: 60/095,486  
; EARLIER FILING DATE: 1998-08-05  
; EARLIER APPLICATION NUMBER: 60/096,319  
; EARLIER FILING DATE: 1998-08-12  
; EARLIER APPLICATION NUMBER: 60/095,454  
; EARLIER FILING DATE: 1998-08-06  
; EARLIER APPLICATION NUMBER: 60/095,455  
; EARLIER FILING DATE: 1998-08-06  
; NUMBER OF SEQ ID NOS: 376  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 139  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-489-847-139

Query Match 100.0%; Score 170; DB 4; Length 112;  
Best Local Similarity 100.0%; Pred. No. 8.4e-17;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARGSLRRLRLVGLWLLRLSRVAGEQAPGTAP 35  
Db 1 MARGSLRRLRLVGLWLLRLSRVAGEQAPGTAP 35

RESULT 2  
US-09-690-454-59  
; Sequence 59, Application US/09690454  
; Patent No. 6531447  
; GENERAL INFORMATION:  
; APPLICANT: Steven M. Ruben, et al.  
; TITLE OF INVENTION: 32 Human Secreted Proteins  
; FILE REFERENCE: P2006P1  
; CURRENT APPLICATION NUMBER: US/09/690,454  
; CURRENT FILING DATE: 2000-10-18  
; PRIOR APPLICATION NUMBER: 09/189,144

; PRIOR FILING DATE: 1998-11-10  
; PRIOR APPLICATION NUMBER: 60/044,039  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/048,093  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/048,190  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/050,935  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/048,101  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/048,356  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/056,250  
; PRIOR FILING DATE: August 29, 1997  
; PRIOR APPLICATION NUMBER: 60/056,296  
; PRIOR FILING DATE: August 29, 1997  
; PRIOR APPLICATION NUMBER: 60/056,293  
; PRIOR FILING DATE: August 29, 1997  
; NUMBER OF SEQ ID NOS: 229  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 59  
; LENGTH: 114  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (114)  
; OTHER INFORMATION: Xaa equals stop translation  
US-09-690-454-59

Query Match 100.0%; Score 170; DB 4; Length 114;  
Best Local Similarity 100.0%; Pred. No. 8.5e-17;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARGSLRRLRLVGLVGLWLLRLSVAGEQAPGTAP 35  
Db 1 MARGSLRRLRLVGLVGLWLLRLSVAGEQAPGTAP 35

RESULT 3  
US-09-883-777-4  
; Sequence 4, Application US/09883777  
; Patent No. 6727225  
; GENERAL INFORMATION:  
; APPLICANT: Wiley, Steven R.  
; TITLE OF INVENTION: TWEAK RECEPTOR  
; FILE REFERENCE: 2968-C  
; CURRENT APPLICATION NUMBER: US/09/883,777  
; CURRENT FILING DATE: 2001-06-18  
; PRIOR APPLICATION NUMBER: US 60/172,878  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: US 60/203,347  
; PRIOR FILING DATE: 2000-05-10  
; PRIOR APPLICATION NUMBER: PCT/US00/34755  
; PRIOR FILING DATE: 2000-12-19  
; PRIOR APPLICATION NUMBER: US 09/742,454  
; PRIOR FILING DATE: 2000-12-19  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 4  
; LENGTH: 129  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-09-883-777-4

Query Match 100.0%; Score 170; DB 4; Length 129;  
Best Local Similarity 100.0%; Pred. No. 9.7e-17;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARGSLRRLRLVGLVGLWLLRLSVAGEQAPGTAP 35  
Db 1 MARGSLRRLRLVGLVGLWLLRLSVAGEQAPGTAP 35

RESULT 4  
US-09-949-016-6914  
; Sequence 4, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6914  
; LENGTH: 129  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-6914

Query Match 100.0%; Score 170; DB 4; Length 129;  
Best Local Similarity 100.0%; Pred. No. 9.7e-17;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARGSLRRLRLVGLVGLWLLRLSVAGEQAPGTAP 35  
Db 1 MARGSLRRLRLVGLVGLWLLRLSVAGEQAPGTAP 35

RESULT 5  
US-09-742-454A-4  
; Sequence 4, Application US/09742454A  
; Patent No. 6824773  
; GENERAL INFORMATION:  
; APPLICANT: WILEY, Steven R.  
; TITLE OF INVENTION: TWEAK Receptor  
; FILE REFERENCE: 2968-B  
; CURRENT APPLICATION NUMBER: US/09/742,454A  
; CURRENT FILING DATE: 2000-12-19  
; PRIOR APPLICATION NUMBER: 60/172,878  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: 60/203,347  
; PRIOR FILING DATE: 2000-05-10  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 129  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-742-454A-4

Query Match 100.0%; Score 170; DB 4; Length 129;  
Best Local Similarity 100.0%; Pred. No. 9.7e-17;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARGSLRRLRLVGLVGLWLLRLSVAGEQAPGTAP 35  
Db 1 MARGSLRRLRLVGLVGLWLLRLSVAGEQAPGTAP 35

RESULT 6  
US-09-489-847-284  
; Sequence 284, Application US/09489847  
; Patent No. 6476195  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al



;; TITLE OF INVENTION: 98 Human Secreted Proteins  
;; FILE REFERENCE: P2031P1  
;; CURRENT APPLICATION NUMBER: US/09/489,847  
;; EARLIER FILING DATE: 2000-01-24  
;; EARLIER APPLICATION NUMBER: PCT/US99/17130  
;; EARLIER FILING DATE: 1999-07-29  
;; EARLIER APPLICATION NUMBER: 60/094,657  
;; EARLIER FILING DATE: 1998-07-30  
;; EARLIER APPLICATION NUMBER: 60/095,486  
;; EARLIER FILING DATE: 1998-08-05  
;; EARLIER APPLICATION NUMBER: 60/096,319  
;; EARLIER FILING DATE: 1998-08-12  
;; EARLIER APPLICATION NUMBER: 60/095,454  
;; EARLIER FILING DATE: 1998-08-06  
;; EARLIER APPLICATION NUMBER: 60/095,455  
;; EARLIER FILING DATE: 1998-08-06  
;; NUMBER OF SEQ ID NOS: 376  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 284  
;; LENGTH: 155  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-09-489-847-284

Query Match 100.0%; Score 170; DB 4; Length 155;  
Best Local Similarity 100.0%; Pred. No. 1.2e-16;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAP 35  
|||||  
Db 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAP 35  
|||||

## RESULT 7

US-09-489-847-228  
;; Sequence 228, Application US/09489847  
;; Patent No. 6476195  
;; GENERAL INFORMATION:

;; APPLICANT: Rosen et al  
;; TITLE OF INVENTION: 98 Human Secreted Proteins  
;; FILE REFERENCE: P2031P1  
;; CURRENT APPLICATION NUMBER: US/09/489,847  
;; EARLIER FILING DATE: 2000-01-24  
;; EARLIER APPLICATION NUMBER: PCT/US99/17130  
;; EARLIER FILING DATE: 1999-07-29  
;; EARLIER APPLICATION NUMBER: 60/094,657  
;; EARLIER FILING DATE: 1998-07-30  
;; EARLIER APPLICATION NUMBER: 60/095,486  
;; EARLIER FILING DATE: 1998-08-05  
;; EARLIER APPLICATION NUMBER: 60/096,319  
;; EARLIER FILING DATE: 1998-08-12  
;; EARLIER APPLICATION NUMBER: 60/095,454  
;; EARLIER FILING DATE: 1998-08-06  
;; EARLIER APPLICATION NUMBER: 60/095,455  
;; EARLIER FILING DATE: 1998-08-06  
;; NUMBER OF SEQ ID NOS: 376  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 228  
;; LENGTH: 156  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens

;; NAME/KEY: SITE  
;; LOCATION: (156)  
;; OTHER INFORMATION: Xaa equals stop translation  
US-09-489-847-228

Query Match 100.0%; Score 170; DB 4; Length 156;  
Best Local Similarity 100.0%; Pred. No. 1.2e-16;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAP 35  
|||||

Db 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAP 35  
|||||

## RESULT 8

US-09-883-777-9  
;; Sequence 9, Application US/09883777  
;; Patent No. 6727225  
;; GENERAL INFORMATION:  
;; APPLICANT: Wiley, Steven R.  
;; TITLE OF INVENTION: TWEAK RECEPTOR  
;; FILE REFERENCE: 2968-C  
;; CURRENT APPLICATION NUMBER: US/09/883,777  
;; EARLIER FILING DATE: 2001-06-18  
;; EARLIER APPLICATION NUMBER: US 60/172,878  
;; EARLIER FILING DATE: 1999-12-20  
;; EARLIER APPLICATION NUMBER: US 60/203,347  
;; EARLIER FILING DATE: 2000-05-10  
;; EARLIER APPLICATION NUMBER: PCT/US00/34755  
;; EARLIER FILING DATE: 2000-12-19  
;; EARLIER APPLICATION NUMBER: US 09/742,454  
;; EARLIER FILING DATE: 2000-12-19  
;; NUMBER OF SEQ ID NOS: 16  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 9  
;; LENGTH: 300  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Human TWEAK receptor fusion protein construct  
US-09-883-777-9

Query Match 100.0%; Score 170; DB 4; Length 300;  
Best Local Similarity 100.0%; Pred. No. 2.4e-16;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAP 35  
|||||  
Db 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAP 35  
|||||

## RESULT 9

US-09-883-777-7  
;; Sequence 7, Application US/09883777  
;; Patent No. 6727225  
;; GENERAL INFORMATION:  
;; APPLICANT: Wiley, Steven R.  
;; TITLE OF INVENTION: TWEAK RECEPTOR  
;; FILE REFERENCE: 2968-C  
;; CURRENT APPLICATION NUMBER: US/09/883,777  
;; EARLIER FILING DATE: 2001-06-18  
;; EARLIER APPLICATION NUMBER: US 60/172,878  
;; EARLIER FILING DATE: 1999-12-20  
;; EARLIER APPLICATION NUMBER: US 60/203,347  
;; EARLIER FILING DATE: 2000-05-10  
;; EARLIER APPLICATION NUMBER: PCT/US00/34755  
;; EARLIER FILING DATE: 2000-12-19  
;; EARLIER APPLICATION NUMBER: US 09/742,454  
;; EARLIER FILING DATE: 2000-12-19  
;; NUMBER OF SEQ ID NOS: 16  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 7  
;; LENGTH: 309  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Human TWEAK receptor fusion protein construct  
US-09-883-777-7

Query Match 100.0%; Score 170; DB 4; Length 309;  
Best Local Similarity 100.0%; Pred. No. 2.5e-16;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARGSLRRLRLVGLWLLALLRSVAGEQAPGTAP 35  
|||||

Db 1 MARGSLRLLRLVLGLWLLALLRSVAGEQAPGTAP 35  
|||||

## RESULT 10

US-09-742-454A-7

; Sequence 7, Application US/09742454A

; Patent No. 6824773

; GENERAL INFORMATION:

; APPLICANT: WILEY, Steven R.

; TITLE OF INVENTION: TWEAK Receptor

; FILE REFERENCE: 2968-B

; CURRENT APPLICATION NUMBER: US/09/742,454A

; CURRENT FILING DATE: 2000-12-19

; PRIOR APPLICATION NUMBER: 60/172,878

; PRIOR FILING DATE: 1999-12-20

; PRIOR APPLICATION NUMBER: 60/203,347

; PRIOR FILING DATE: 2000-05-10

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 7

; LENGTH: 309

; TYPE: PRT

; ORGANISM: Artificial Sequence

; OTHER INFORMATION: Description of Artificial Sequence: human TWEAK  
receptor fusion protein construct

US-09-742-454A-7

Query Match 100.0%; Score 170; DB 4; Length 309;

Best Local Similarity 100.0%; Pred. No. 2.5e-16;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARGSLRLLRLVLGLWLLALLRSVAGEQAPGTAP 35  
|||||Db 1 MARGSLRLLRLVLGLWLLALLRSVAGEQAPGTAP 35  
|||||

## RESULT 11

US-09-883-777-5

; Sequence 5, Application US/09883777

; Patent No. 6727225

; GENERAL INFORMATION:

; APPLICANT: WILEY, Steven R.

; TITLE OF INVENTION: TWEAK RECEPTOR

; FILE REFERENCE: 2968-C

; CURRENT APPLICATION NUMBER: US/09/883,777

; CURRENT FILING DATE: 2001-06-18

; PRIOR APPLICATION NUMBER: US 60/172,878

; PRIOR FILING DATE: 1999-12-20

; PRIOR APPLICATION NUMBER: US 60/203,347

; PRIOR FILING DATE: 2000-05-10

; PRIOR APPLICATION NUMBER: PCT/US00/34755

; PRIOR FILING DATE: 2000-12-19

; PRIOR APPLICATION NUMBER: US 09/742,454

; PRIOR FILING DATE: 2000-12-19

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: Patentin version 3.1

; SEQ ID NO 5

; LENGTH: 129

; TYPE: PRT

; ORGANISM: Mus sp.

US-09-883-777-5

Query Match

Best Local Similarity 57.1%; Score 97; DB 4; Length 129;

Matches 21; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MARGSLRLLRLVLGLWLLALLRSVAGEQAPGTAP 35  
|||||Db 1 MARGSLRLLRLVLGLWLLALLRSVAGEQAPGTSP 35  
|||||

## RESULT 12

US-09-742-454A-5

; Sequence 5, Application US/09742454A

; Patent No. 6824773

; GENERAL INFORMATION:

; APPLICANT: WILEY, Steven R.

; TITLE OF INVENTION: TWEAK Receptor

; FILE REFERENCE: 2968-B

; CURRENT APPLICATION NUMBER: US/09/742,454A

; CURRENT FILING DATE: 2000-12-19

; PRIOR APPLICATION NUMBER: 60/172,878

; PRIOR FILING DATE: 1999-12-20

; PRIOR APPLICATION NUMBER: 60/203,347

; PRIOR FILING DATE: 2000-05-10

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: Patentin Ver. 2.0

; SEQ ID NO 5

; LENGTH: 129

; TYPE: PRT

; ORGANISM: Mus sp.

US-09-742-454A-5

Query Match 57.1%; Score 97; DB 4; Length 129;

Best Local Similarity 60.0%; Pred. No. 2.5e-06;

Matches 21; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MARGSLRLLRLVLGLWLLALLRSVAGEQAPGTAP 35  
|||||Db 1 MARGSLRLLRLVLGLWLLALLRSVAGEQAPGTSP 35  
|||||

## RESULT 13

US-09-949-016-7892

; Sequence 7892, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: C0001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 7892

; LENGTH: 1217

; TYPE: PRT

; ORGANISM: Human

US-09-949-016-7892

Query Match

Best Local Similarity 32.1%; Score 54.5; DB 4; Length 1217;

Matches 14; Conservative 1; Mismatches 12; Indels 1; Gaps 1;

Qy 9 LLRLVLGLW-LALLRSVAGEQAPGTAP 35  
|||||Db 1184 LLALLVLALWKLGFPRSRARRRREGGLDP 1211  
|||||

## RESULT 14

US-09-254-465A-10

; Sequence 10, Application US/09254465A

; Patent No. 6410708

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Fong, Sherman

```

; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Napier, Mary A.
; APPLICANT: Tomas, Daniel
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: COMPOUNDS, COMPOSITIONS AND METHODS FOR THE TREATMENT
; OF DISEASES CHARACTERIZED BY A33- RELATED ANTIGENS
; FILE REFERENCE: P1216R1(US)
; CURRENT APPLICATION NUMBER: US/09/254,465A
; PRIOR FILING DATE: 1999-03-05
; PRIOR APPLICATION NUMBER: PCT/US98/24855
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: US 60/066,364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: US 60/078,936
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: PCT/US98/19437
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 30
; SEQ ID NO 10
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-254-465A-10

```

```

Query Match 31.8%; Score 54; DB 4; Length 300;
Best Local Similarity 44.4%; Pred. No. 8.1;
Matches 12; Conservative 2; Mismatches 13; Indels 0; Gaps 0;

```

```

QY 9 LRLVLGLWLLRSVAGEQAPGTAP 35
|||:|:|:|:|
DB 249 LIGLLIFGVWFAYSRGYFETTKGTAP 275

```

```

RESULT 15
US-09-397-243D-12
; Sequence 12, Application US/09397243D
; Patent No. 6699688
; GENERAL INFORMATION:
; APPLICANT: Kornecki, Elizabeth
; APPLICANT: Sobocka, Malgorzata B.
; TITLE OF INVENTION: Human Platelet F11 Receptor
; FILE REFERENCE: 011.00221
; CURRENT APPLICATION NUMBER: US/09/397,243D
; PRIOR FILING DATE: 1999-09-16
; PRIOR APPLICATION NUMBER: 60/100,638
; PRIOR FILING DATE: 1998-09-16
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-397-243D-12

```

```

Query Match 31.8%; Score 54; DB 4; Length 300;
Best Local Similarity 44.4%; Pred. No. 8.1;
Matches 12; Conservative 2; Mismatches 13; Indels 0; Gaps 0;

```

```

QY 9 LRLVLGLWLLRSVAGEQAPGTAP 35
|||:|:|:|:|
DB 249 LIGLLIFGVWFAYSRGYFETTKGTAP 275

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Search completed: February 10, 2005, 18:18:45
Job time : 15.4298 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2005, 18:03:08 ; Search time 10.2851 Seconds  
(without alignments)  
327.424 Million cell updates/sec

Title: US-10-062-831-59\_COPY\_36\_70

Perfect score: 203

Sequence: 1 CSRGSSWSADLDKCMDCASCRRPHSDFCLGCAAA 35

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	64	31.5	261	2 G69099	probable pyruvate
2	63.5	31.3	893	2 S51603	receptor-like tyro
3	63.5	31.3	898	2 S47489	receptor tyrosine
4	63.5	31.3	981	2 S51604	receptor-like tyro
5	63.5	31.3	1005	2 S49015	receptor tyrosine
6	61	30.0	390	2 F69086	pyruvate formate-1
7	60.5	29.8	76	2 T03860	TA20 protein - com
8	59.5	29.3	414	2 T15947	hypothetical prote
9	59.5	29.3	431	1 B69092	conserved hypothet
10	59.5	29.3	1013	2 I50615	receptor-type prot
11	59.5	29.3	1210	1 GQHUE	epidermal growth f
12	59	29.1	55	1 FEPE	ferredoxin 2[4Fe-4
13	58.5	28.8	1210	2 A53183	epidermal growth f
14	58.5	28.8	1548	2 S34583	serine proteinase
15	58	28.6	197	2 T50025	hypothetical prote
16	57.5	28.3	644	2 A36325	epidermal growth f
17	56	27.6	103	2 T08775	hypothetical prote
18	56	27.6	2871	2 A55624	fibrillin-1 precu
19	55.5	27.3	59	1 FEDV2N	ferredoxin 2[4Fe-4
20	55.5	27.3	991	2 I78843	receptor protein-t
21	54.5	26.8	464	2 S48329	probable membrane
22	54.5	26.8	560	2 T16833	hypothetical prote
23	54.5	26.8	932	2 I52527	PACE4A - mouse
24	54	26.6	421	1 H0DVLV	cytochrome-c3 hydr
25	53.5	26.4	97	2 H82120	ferredoxin (import
26	53.5	26.4	281	2 H84263	chloromuconate cyc
27	53	26.1	63	2 C69303	ferredoxin (fdx-4)
28	53	26.1	286	2 T49505	hypothetical prote
29	53	26.1	319	2 E84528	hypothetical prote

30	53	26.1	319	2 S71177	DNA-directed RNA p
31	53	26.1	366	2 I53035	trithorax homolog
32	53	26.1	558	2 I56545	glypican precursor
33	53	26.1	1221	2 A49457	fibulin-2 precursor
34	53	26.1	3869	2 A48205	All-1 protein +GTE
35	53	26.1	3968	2 A44285	trithorax homolog
36	52.5	25.9	58	2 C69365	ferredoxin (fdx-5)
37	52.5	25.9	1255	1 A24571	protein-tyrosine k
38	52	25.6	81	2 A45320	transglutaminase s
39	52	25.6	589	2 T43210	fibulin-1D precurs
40	52	25.6	669	2 S65551	factor H - bovine
41	52	25.6	689	2 T42760	fibulin, aplice fo
42	52	25.6	712	2 T42990	fibulin 1, splice
43	52	25.6	798	2 T22793	hypothetical prote
44	52	25.6	1107	2 T15884	hypothetical prote
45	51.5	25.4	346	2 S62197	molybdenum formylm

#### ALIGNMENTS

##### RESULT 1

G69099

probable pyruvate synthase (EC 1.2.7.1) gamma chain - Methanobacterium thermoautotrophic

C;Species: Methanobacterium thermoautotrophicum

C;Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 05-May-2000

C;Accession: G69099

R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;

Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiواني, N.

Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.

J. Bacteriol. 179, 7135-7155, 1997

A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct

A;Reference number: A69000; MUID:98037514; PMID:9371463

A;Accession: G69099

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-261 <MTH>

A;Cross-references: GB:AR0000929; GB:AR000666; NID:G2622853; PIDN:AAB86210.1; PID:G262287

A;Experimental source: strain Delta H

C;Genetics:

A;Gene: MTH1740

C;Superfamily: pyruvate synthase gamma chain

C;Keywords: coenzyme A; oxidoreductase

Query Match 31.5%; Score 64; DB 2; Length 261;  
Best Local Similarity 31.9%; Pred. No. 1.7;  
Matches 15; Conservative 5; Mismatches 11; Indels 16; Gaps 3;

Qy 2 SRGSSWSA-----DLDKCMDCASCRA-----RPHS---DFCLGC 32  
::|||::|  
Db 197 NKTGSWRTFKPVLDKDKICIDCNCILFCPEGCINREHIDYCKGC 243  
::|||::|

##### RESULT 2

S51603

receptor-like tyrosine kinase Etk-1 - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 07-May-1995 #sequence\_revision 21-Jul-1995 #text\_change 09-Jul-2004

C;Accession: S51603

R;Maisongier, P.C.; Barrezaeta, N.X.; Yancopoulos, G.D.

Oncogene 8, 3277-3288, 1993

A;Title: Etk-1 and Etk-2: two novel members of the Eph receptor-like tyrosine kinase fam

A;Reference number: S49015; MUID:94067777; PMID:7504232

A;Accession: S51603

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-893 <MAI>

A;Cross-references: UNIPROT:P54757; EMBL:S68028

A;Note: the authors translated the codon GAC for residue 170 as Glu

C;Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h

C;Keywords: ATP; transmembrane protein

F;563-829/Domain: protein kinase homology <KIN>

F;571-579/Region: protein kinase ATP-binding motif

Query Match 31.3%; Score 63.5; DB 2; Length 893;  
Best Local Similarity 31.9%; Pred. No. 4.8;  
Matches 15; Conservative 1; Mismatches 16; Indels 15; Gaps 2;

Qy 1 CSRGSSWSADLDKCM-----DCASCR-----ARPHSDFCLGCG 32  
Db 278 CSAEGEWLVPIGCKMCKAGYEKNGTCQVCRPGFFKASPHSQTSKCK 324

RESULT 3  
S47489  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 18-Jun-1999  
C:Accession: S47489  
R:Taylor, V.; Priar, S.; Miescher, G.C.; Honegger, P.; Breitschopf, H.; Laessmann, H.; St  
submitted to the EMBL Data Library, April 1994  
A:Description: Expression and developmental regulation of EHK-1, a neuronal ELK-like rec  
A:Reference number: S47489  
A:Accession: S47489  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-898 <TA>  
A:Cross-references: EMBL:X78689; NID:G531543; PIDN:CAA55357.1; PID:G531544  
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h  
C:Keywords: ATP; transmembrane protein  
F:568-834/Domain: protein kinase homology <KIN>  
F:576-584/Region: protein kinase ATP-binding motif

Query Match 31.3%; Score 63.5; DB 2; Length 898;  
Best Local Similarity 31.9%; Pred. No. 4.8;  
Matches 15; Conservative 1; Mismatches 16; Indels 15; Gaps 2;

Qy 1 CSRGSSWSADLDKCM-----DCASCR-----ARPHSDFCLGCG 32  
Db 283 CSAEGEWLVPIGCKMCKAGYEKNGTCQVCRPGFFKASPHSQTSKCK 329

RESULT 4  
S51604  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 07-May-1995 #sequence\_revision 21-Jul-1995 #text\_change 29-May-1998  
C:Accession: S51604  
R:Maisonpierre, P.C.; Barreuzeta, N.X.; Yancopoulos, G.D.  
Oncogene 8, 3277-3288, 1993  
A:Title: EHK-1 and EHK-2: two novel members of the Eph receptor-like tyrosine kinase fa  
A:Reference number: S49015; MUID:94067777; PMID:7504232  
A:Accession: S51604  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-981 <MAI>  
A:Cross-references: EMBL:S68029  
A:Note: the authors translated the codon GAC for residue 170 as Glu  
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h  
C:Keywords: ATP; transmembrane protein  
F:651-917/Domain: protein kinase homology <KIN>  
F:659-667/Region: protein kinase ATP-binding motif

Query Match 31.3%; Score 63.5; DB 2; Length 981;  
Best Local Similarity 31.9%; Pred. No. 5.2;  
Matches 15; Conservative 1; Mismatches 16; Indels 15; Gaps 2;

Qy 1 CSRGSSWSADLDKCM-----DCASCR-----ARPHSDFCLGCG 32  
Db 278 CSAEGEWLVPIGCKMCKAGYEKNGTCQVCRPGFFKASPHSQTSKCK 324

RESULT 5  
S49015  
C:Species: Rattus norvegicus (Norway rat)

C:Date: 14-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 09-Jul-2004  
C:Accession: S49015; S51602  
R:Maisonpierre, P.C.; Barreuzeta, N.X.; Yancopoulos, G.D.  
Oncogene 8, 3277-3288, 1993  
A:Title: EHK-1 and EHK-2: two novel members of the Eph receptor-like tyrosine kinase fa  
A:Reference number: S49015; MUID:94067777; PMID:7504232  
A:Accession: S49015  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1005 <MAI>  
A:Cross-references: UNIPROT:P54757; EMBL:S68024  
A:Note: the authors translated the codon GAC for residue 170 as Glu  
A:Accession: S51602  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-305; G', 359-1005 <MA2>  
A:Cross-references: EMBL:S68026  
A:Note: the authors translated the codon GAC for residue 170 as Glu  
C:Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h  
C:Keywords: ATP; transmembrane protein  
F:675-941/Domain: protein kinase homology <KIN>  
F:683-691/Region: protein kinase ATP-binding motif

Query Match 31.3%; Score 63.5; DB 2; Length 1005;  
Best Local Similarity 31.9%; Pred. No. 5.3;  
Matches 15; Conservative 1; Mismatches 16; Indels 15; Gaps 2;

Qy 1 CSRGSSWSADLDKCM-----DCASCR-----ARPHSDFCLGCG 32  
Db 278 CSAEGEWLVPIGCKMCKAGYEKNGTCQVCRPGFFKASPHSQTSKCK 324

RESULT 6  
F69086  
pyruvate formate-lyase activating enzyme related protein - Methanobacterium thermoautotr  
C:Species: Methanobacterium thermoautotrophicum  
C:Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
C:Accession: F69086  
R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;  
Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiواني, N.;  
Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.  
J. Bacteriol. 179, 7135-7155, 1997  
A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct  
A:Reference number: A69000; MUID:98037514; PMID:9371463  
A:Accession: F69086  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-390 <MTH>  
A:Cross-references: UNIPROT:O27680; GB:AE000923; GB:AE000666; NID:G2622766; PIDN:AAB8611.  
A:Experimental source: strain Delta H  
C:Genetics:  
A:Gene: MTH1643  
A:Start codon: GTG

Query Match 30.0%; Score 61; DB 2; Length 390;  
Best Local Similarity 43.5%; Pred. No. 5.2;  
Matches 10; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

Qy 12 DKCWDACSCARPHSDFCLGCA 34  
Db 14 DRCRCGNCRELKCSNCTGCRA 36

RESULT 7  
T03860  
TA20 protein - common tobacco  
C:Species: Nicotiana tabacum (common tobacco)  
C:Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
C:Accession: T03860  
R:Beals, T.P.; Goldberg, R.B.  
submitted to the EMBL Data Library, October 1996  
A:Description: Nicotiana tabacum gene expressed in anther.  
A:Reference number: Z15122

Query Match 29.3%; Score 59.5; DB 1; Length 431;  
Best Local Similarity 32.6%; Pred. No. 8.4;  
Matches 14; Conservative 4; Mismatches 8; Indels 17; Gaps 3;

epidermal growth factor receptor precursor - human  
N;Contains: protein-tyrosine kinase (EC 2.7.1.112) erbB  
C;Species: Homo sapiens (man)  
C;Date: 15-Nov-1994 #sequence revision 27-Nov-1985 #text change 09-Jul-2004  
C;Accession: A00641; A25772; S30024; A38672; A00642; A43615; A23062; A05281; A60143; A33333; A33334; A33335; A33336; A33337; A33338; A33339; A33340; A33341; A33342; A33343; A33344; A33345; A33346; A33347; A33348; A33349; A33350; A33351; A33352; A33353; A33354; A33355; A33356; A33357; A33358; A33359; A33360; A33361; A33362; A33363; A33364; A33365; A33366; A33367; A33368; A33369; A33370; A33371; A33372; A33373; A33374; A33375; A33376; A33377; A33378; A33379; A33380; A33381; A33382; A33383; A33384; A33385; A33386; A33387; A33388; A33389; A33390; A33391; A33392; A33393; A33394; A33395; A33396; A33397; A33398; A33399; A33400; A33401; A33402; A33403; A33404; A33405; A33406; A33407; A33408; A33409; A33410; A33411; A33412; A33413; A33414; A33415; A33416; A33417; A33418; A33419; A33420; A33421; A33422; A33423; A33424; A33425; A33426; A33427; A33428; A33429; A33430; A33431; A33432; A33433; A33434; A33435; A33436; A33437; A33438; A33439; A33440; A33441; A33442; A33443; A33444; A33445; A33446; A33447; A33448; A33449; A33450; A33451; A33452; A33453; A33454; A33455; A33456; A33457; A33458; A33459; A33460; A33461; A33462; A33463; A33464; A33465; A33466; A33467; A33468; A33469; A33470; A33471; A33472; A33473; A33474; A33475; A33476; A33477; A33478; A33479; A33480; A33481; A33482; A33483; A33484; A33485; A33486; A33487; A33488; A33489; A33490; A33491; A33492; A33493; A33494; A33495; A33496; A33497; A33498; A33499; A33500; A33501; A33502; A33503; A33504; A33505; A33506; A33507; A33508; A33509; A33510; A33511; A33512; A33513; A33514; A33515; A33516; A33517; A33518; A33519; A33520; A33521; A33522; A33523; A33524; A33525; A33526; A33527; A33528; A33529; A33530; A33531; A33532; A33533; A33534; A33535; A33536; A33537; A33538; A33539; A33540; A33541; A33542; A33543; A33544; A33545; A33546; A33547; A33548; A33549; A33550; A33551; A33552; A33553; A33554; A33555; A33556; A33557; A33558; A33559; A33560; A33561; A33562; A33563; A33564; A33565; A33566; A33567; A33568; A33569; A33570; A33571; A33572; A33573; A33574; A33575; A33576; A33577; A33578; A33579; A33580; A33581; A33582; A33583; A33584; A33585; A33586; A33587; A33588; A33589; A33590; A33591; A33592; A33593; A33594; A33595; A33596; A33597; A33598; A33599; A33600; A33601; A33602; A33603; A33604; A33605; A33606; A33607; A33608; A33609; A33610; A33611; A33612; A33613; A33614; A33615; A33616; A33617; A33618; A33619; A33620; A33621; A33622; A33623; A33624; A33625; A33626; A33627; A33628; A33629; A33630; A33631; A33632; A33633; A33634; A33635; A33636; A33637; A33638; A33639; A33640; A33641; A33642; A33643; A33644; A33645; A33646; A33647; A33648; A33649; A33650; A33651; A33652; A33653; A33654; A33655; A33656; A33657; A33658; A33659; A33660; A33661; A33662; A33663; A33664; A33665; A33666; A33667; A33668; A33669; A33670; A33671; A33672; A33673; A33674; A33675; A33676; A33677; A33678; A33679; A33680; A33681; A33682; A33683; A33684; A33685; A33686; A33687; A33688; A33689; A33690; A33691; A33692; A33693; A33694; A33695; A33696; A33697; A33698; A33699; A33700; A33701; A33702; A33703; A33704; A33705; A33706; A33707; A33708; A33709; A33710; A33711; A33712; A33713; A33714; A33715; A33716; A33717; A33718; A33719; A33720; A33721; A33722; A33723; A33724; A33725; A33726; A33727; A33728; A33729; A33730; A33731; A33732; A33733; A33734; A33735; A33736; A33737; A33738; A33739; A33740; A33741; A33742; A33743; A33744; A33745; A33746; A33747; A33748; A33749; A33750; A33751; A33752; A33753; A33754; A33755; A33756; A33757; A33758; A33759; A33760; A33761; A33762; A33763; A33764; A33765; A33766; A33767; A33768; A33769; A33770; A33771; A33772; A33773; A33774; A33775; A33776; A33777; A33778; A33779; A33780; A33781; A33782; A33783; A33784; A33785; A33786; A33787; A33788; A33789; A33790; A33791; A33792; A33793; A33794; A33795; A33796; A33797; A33798; A33799; A33800; A33801; A33802; A33803; A33804; A33805; A33806; A33807; A33808; A33809; A33810; A33811; A33812; A33813; A33814; A33815; A33816; A33817; A33818; A33819; A33820; A33821; A33822; A33823; A33824; A33825; A33826; A33827; A33828; A33829; A33830; A33831; A33832; A33833; A33834; A33835; A33836; A33837; A33838; A33839; A33840; A33841; A33842; A33843; A33844; A33845; A33846; A33847; A33848; A33849; A33850; A33851; A33852; A33853; A33854; A33855; A33856; A33857; A33858; A33859; A33860; A33861; A33862; A33863; A33864; A33865; A33866; A33867; A33868; A33869; A33870; A33871; A33872; A33873; A33874; A33875; A33876; A33877; A33878; A33879; A33880; A33881; A33882; A33883; A33884; A33885; A33886; A33887; A33888; A33889; A33890; A33891; A33892; A33893; A33894; A33

A;Cross-references: GB:M11234; NID:g181981; PIDN:AA52370.1; PID:g553272  
R;Haley, J.; Whittle, N.; Bennett, P.; Kinchington, D.; Ulrich, A.; Waterfield, M.  
Oncogene Res. 1, 375-396, 1987  
A;Title: The human EGF receptor gene: structure of the 110 kb locus and identification of  
A;Reference number: S30024; MUID:88217333; PMID:3329716  
A;Accession: S30024  
A;Molecule type: DNA  
A;Residues: 1-29 <HA2>  
A;Cross-references: EMBL:X06370; NID:g31118; PIDN:CAA29668.1; PID:g31119  
R;Haley, J.D.; Waterfield, M.D.  
J. Biol. Chem. 266, 1746-1753, 1991  
A;Title: Contributory effects of de Novo transcription and premature transcript termination  
A;Reference number: A38672; MUID:91107677; PMID:1988448  
A;Accession: A38672  
A;Molecule type: DNA  
A;Residues: 1-29 <HAL>  
A;Cross-references: GB:M38425; NID:g181977; PIDN:AAA63171.1; PID:g553271  
A;Experimental source: carcinoma cell line A431-7  
R;Xu, Y.; Tahii, S.; Clark, A.J.L.; Sullivan, M.; Wilson, R.K.; Ma, D.P.; Roe, B.A.; Meier  
Nature 309, 806-810, 1984  
A;Title: Human epidermal growth factor receptor cDNA is homologous to a variety of RNAs  
A;Reference number: A00642; MUID:84245835; PMID:6330563  
A;Accession: A00642  
A;Molecule type: mRNA  
A;Residues: 'RCAWRRA', 150-187, 'KSVIQAV', 195, 'M', 197, 'A', 199-222, 'S', 224-304, 'RA', 307-321  
', 798-799, 'TD', 802-811, 'R', 813-942 <XY>  
A;Experimental source: A431 human carcinoma cells, which have large numbers of EGF receptor  
R;Lin, C.R.; Chen, W.S.; Krueger, W.; Stolarsky, L.S.; Weber, W.; Evans, R.M.; Verma, I.  
Science 224, 843-848, 1984  
A;Title: Expression cloning of human EGF receptor complementary DNA: gene amplification  
A;Reference number: A43615; MUID:84196372; PMID:6326261  
A;Accession: A43615  
A;Molecule type: mRNA  
A;Residues: 713-964 <LIN>  
A;Experimental source: epidermoid carcinoma cell line A431  
R;Simmen, F.A.; Gope, M.L.; Schulz, T.Z.; Wright, D.A.; Carpenter, G.; O'Malley, B.W.  
Biochem. Biophys. Res. Commun. 124, 125-132, 1984  
A;Reference number: A23062; MUID:85046483; PMID:6093780  
A;Accession: A23062  
A;Molecule type: mRNA  
A;Residues: 1028-1210 <SIM>  
R;Weber, W.; Gill, G.N.; Speiss, J.  
Science 224, 294-297, 1984  
A;Reference number: A05281; MUID:84172183; PMID:6324343  
A;Accession: A05281  
A;Molecule type: protein  
A;Residues: 25-30, 'S', 32-51, 454-467 <WEB>  
R;Russo, M.W.; Lukas, T.J.; Cohen, S.; Staros, J.V.  
J. Biol. Chem. 260, 5205-5208, 1985  
A;Title: Identification of residues in the nucleotide binding site of the epidermal growth  
A;Reference number: A60143; MUID:85182650; PMID:2985580  
A;Accession: A60143  
A;Molecule type: protein  
A;Residues: 740-744, 'X', 746-747 <RUS>  
R;Mroczkowski, B.; Mosig, G.; Cohen, S.  
Nature 309, 270-273, 1984  
A;Title: ATP-stimulated interaction between epidermal growth factor receptor and superoxide  
A;Reference number: A38023; MUID:84191554; PMID:6325948  
A;Contents: annotation; receptor activity  
A;Note: the EGF receptor (and other tyrosine kinases) can nick double-stranded DNA  
R;Chen, W.S.; Lazar, C.S.; Lund, K.A.; Welsh, J.B.; Chang, C.P.; Walton, G.M.; Der, C.J.  
Cell 59, 33-43, 1989  
A;Title: Functional independence of the epidermal growth factor receptor from a domain 2  
A;Reference number: A3331; MUID:90003233; PMID:2790960  
A;Contents: annotation; internalization signal  
A;Comment: Binding of EGF to the receptor leads to internalization of the EGF-receptor complex  
C;Genetics:  
A;Gene: GDB:EGFR  
A;Cross-references: GDB:120610; OMIM:131550  
A;Map position: 7p12.3-7p12.1  
C;Superfamily: epidermal growth factor receptor; protein kinase homology  
C;Keywords: ATP; autophosphorylation; duplication; glycoprotein; phosphoprotein; phosphotyrosine  
F;1-24/Domain: signal sequence #status predicted <SIG>

F;25-1210/Product: EGF receptor #status predicted <MAT>  
F;25-645/Domain: extracellular #status predicted <EXT>  
F;75-300/Domain: EGF receptor extracellular domain repeat <BE1>  
F;390-600/Domain: EGF receptor extracellular domain repeat <BE2>  
F;646-668/Domain: transmembrane #status predicted <TMW>  
F;669-1210/Domain: intracellular #status predicted <INT>  
F;710-975/Domain: protein kinase homology <KIN>  
F;718-726/Region: protein kinase ATP-binding motif  
F;999-1046/Region: coated-pit mediated internalization signal  
F;1047-1210/Region: inhibitory  
F;128,175,352,413,444,528,603/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F;745/Active site: Lys #status experimental

Query Match 29.3%; Score 59.5; DB 1; Length 1210;  
Best Local Similarity 35.6%; Pred. No. 18; Indels 11; Gaps 3;  
Matches 16; Conservative 2; Mismatches 16;

Qy 1 CSRGSSWSADLDKCMD-----CAS-----CRARPHSDFCLG-CAA 34  
Db 194 CPNGSGWAGBENCQKLTIKICQQCSGRCGRKSPSPDCCHNQCAA 238

RESULT 12

FEPE  
ferredoxin 2[4Fe-4S] [validated] - Peptostreptococcus asaccharolyticus  
C;Species: Peptostreptococcus asaccharolyticus  
C;Date: 24-Apr-1984 #sequence\_revision 23-Mar-1995 #text\_change 12-Jul-2004  
C;Accession: A00196  
R;Tsunoda, J.N.; Yasunobu, K.T.; Whiteley, H.R.  
J. Biol. Chem. 243, 6262-6272, 1968  
A;Title: Non-heme iron proteins. IX. The amino acid sequence of ferredoxin from Micrococcus  
A;Reference number: A92040; MUID:69054261; PMID:5723466  
A;Note: the source is designated as Micrococcus aerogenes  
A;Accession: A00196  
A;Molecule type: protein  
A;Residues: 1-21,23-24,'Q',26-55 <TSU>  
A;Cross-references: UNIPROT:P00193  
R;Backes, G.; Mino, Y.; Loehr, T.M.; Meyer, T.E.; Cusanovich, M.A.; Sweeney, W.V.; Adman  
J. Am. Chem. Soc. 113, 2055-2064, 1991  
A;Title: The environment of Fe4S4 clusters in ferredoxins and high-potential iron proteins  
A;Reference number: A44688  
A;Contents: annotation; X-ray crystallography, 2.0 angstroms; sequence revision  
A;Note: sequence correction confirmed by peptide sequencing  
R;Adman, E.T.; Sieker, L.C.; Jensen, L.H.  
submitted to the Brookhaven Protein Data Bank, August 1976  
A;Reference number: A50836; PDB:1FDX  
A;Contents: annotation; X-ray crystallography, 2.0 angstroms, residues 1-21,'I',23-24,26  
R;Adman, E.T.; Sieker, L.C.; Jensen, L.H.  
J. Biol. Chem. 251, 3801-3806, 1976  
A;Title: Structure of Peptococcus aerogenes ferredoxin. Refinement at 2 angstroms resolution  
A;Reference number: A92192; MUID:76213238; PMID:932007  
A;Contents: annotation; X-ray crystallography, 2.0 angstroms  
R;Adman, E.T.; Sieker, L.C.; Jensen, L.H.  
J. Biol. Chem. 248, 3987-3996, 1973  
A;Title: The structure of a bacterial ferredoxin.  
A;Reference number: A92136; MUID:73187389; PMID:4708097  
A;Contents: annotation; X-ray crystallography, 2.8 angstroms  
C;Keywords: 4Fe-4S; electron transfer; iron-sulfur protein; metalloprotein  
F;1-54/Domain: ferredoxin 2[4Fe-4S] homology <FER>  
F;8,11,14,46/Binding site: 4Fe-4S cluster (Cys) (covalent) #status experimental  
F;18,36,39,42/Binding site: 4Fe-4S cluster (Cys) (covalent) #status experimental

Query Match 29.1%; Score 59; DB 1; Length 55;  
Best Local Similarity 52.9%; Pred. No. 2.1; Indels 5; Gaps 0;  
Matches 9; Conservative 3; Mismatches 5;

Qy 4 GSSWSADLDKCMDASC 20  
Db 26 GSIYDAIDADSCIDCGSC 42

RESULT 13  
A53183



epidermal growth factor receptor precursor - mouse

C:Species: Mus musculus (house mouse)  
C>Date: 06-Jan-1995 #sequence revision 06-Jan-1995 #text change 09-Jul-2004  
R:Luetteke, N.C.; Phillips, H.K.; Qiu, T.H.; Copeland, N.G.; Earp, H.S.; Jenkins, N.A.;  
Genes Dev. 8, 399-413, 1994  
A>Title: The mouse waved-2 phenotype results from a point mutation in the EGF receptor  
A:Reference number: A53183; MUID:94170986; PMID:8125255  
A:Accession: A53183  
A:Molecule type: mRNA  
A:Residues: 1-1210 <LUE>  
A:Cross-references: UNIPROT:Q01279; GB:U03425  
R:Avivi, A.; Lax, I.; Ullrich, A.; Schlessinger, J.; Givol, D.; Morse, B.  
Oncogene 6, 673-676, 1991  
A>Title: Comparison of EGF receptor sequences as a guide to study the ligand binding site  
A:Reference number: A43818; MUID:91232866; PMID:2030916  
A:Accession: A43818  
A:Molecule type: mRNA  
A:Residues: 1-714 <AVI>  
A:Cross-references: GB:X59698  
R:Eisinger, D.P.; Serrero, G.  
Submitted to the EMBL Data Library, June 1992  
A:Reference number: S24942  
A:Accession: S24942  
A:Molecule type: mRNA  
A:Residues: 969-971, 'K', 973-1115, 'D' <BIS>  
A:Cross-references: EMBL:Z12608  
R:Heisermann, G.J.; Gill, G.N.  
J. Biol. Chem. 263, 13152-13158, 1988  
A>Title: Epidermal growth factor receptor threonine and serine residues phosphorylated  
A:Reference number: A28941; MUID:88330814; PMID:3138233  
A:Accession: A28941  
A:Molecule type: protein  
A:Residues: 689-694, 'X', 696-704, 'L', 706-707, 989-992, 'XX', 995-996, 'X', 998-1000, 1002-1009,  
R:Hibbs, M.L.; Dunn, A.R.; Alexander, W.S.  
Submitted to the EMBL Data Library, April 1994  
A>Description: The complete cDNA sequence of the Mouse Epidermal Growth Factor Receptor  
A:Reference number: S45325  
A:Accession: S45325  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-971, 'K', 973-1210 <VER>  
A:Cross-references: EMBL:X78987; NID:G488830; PIDN:CAA55587.1; PID:G488831  
R:Paria, B.C.; Das, S.K.; Andrews, G.K.; Dey, S.K.  
Proc. Natl. Acad. Sci. U.S.A. 90, 55-59, 1993  
A>Title: Expression of the epidermal growth factor receptor gene is regulated in mouse  
A:Reference number: I49643; MUID:93126380; PMID:7678348  
A:Accession: I49643  
A>Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 12-20, 22-132 <RES>  
A:Cross-references: GB:L06864; NID:G193001; PIDN:AAA53029.1; PID:G567201  
C:Genetics:  
A:Gene: EGFR  
C:Superfamily: epidermal growth factor receptor; protein kinase homology  
C:Keywords: ATP; growth factor receptor; kinase-related transforming protein; phosphoprotein  
P:1-24/Domain: signal sequence #status predicted <SIG>  
P:648-670/Domain: transmembrane #status predicted <TM>  
P:712-977/Domain: protein kinase homology <KIN>  
P:720-728/Region: protein kinase ATP-binding motif  
F:680,695/Binding site: phosphate (Thr) (covalent) #status experimental  
F:697,1070,1071/Binding site: phosphate (Ser) (covalent) #status experimental  
F:993/Binding site: (or 997) phosphate (Ser) (covalent) #status experimental  
F:1028/Binding site: (or 1030 or 1032) phosphate (Ser) (covalent) #status experimental  
F:1197/Binding site: phosphate (Tyr) (covalent) #status experimental

Query Match 28.8%; Score 58.5; DB 2; Length 1210;  
Best Local Similarity 35.6%; Pred. No. 24;  
Matches 16; Conservative 1; Mismatches 17; Indels 11; Gaps 3;

QY 1 CSRGSSWADLDKCMD-----CAS-----CRPHSDFLCG-CAA 34

DB 194 CPNGSCWGGGEECQKLTIIICAAQCRCRGRSPSCDCNQCAA 238

#### RESULT 14

S34583

serine proteinase (EC 3.4.21.-) PC6B - mouse

C:Species: Mus musculus (house mouse)

C>Date: 02-Dec-1993 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004

C:Accession: S34583

R:Nakagawa, T.; Murakami, K.; Nakayama, K.

PEBS Lett. 327, 165-171, 1993

A>Title: Identification of an isoform with an extremely large Cys-rich region of PC6, a

A:Reference number: S34583; MUID:93327934; PMID:8335106

A:Accession: S34583

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1548 <NAK>

A:Cross-references: UNIPROT:Q04592; GB:D17583; NID:G407344; PIDN:BAA04507.1; PID:dl100503

C:Keywords: hydrolase; serine proteinase

Query Match 28.8%; Score 58.5; DB 2; Length 1548;

Best Local Similarity 40.0%; Pred. No. 28;

Matches 14; Conservative 3; Mismatches 15; Indels 3; Gaps 2;

QY 1 CSRGSSWADLDKCMD-ASCRA--RPHSDFLCG 32

DB 1201 CPEGYHTDKSQCVLCHSSCRCEGPHSMQCLSC 1235

#### RESULT 15

T50025

hypothetical protein T31P16.200 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Jun-2000 #sequence\_revision 02-Jun-2000 #text\_change 09-Jul-2004

C:Accession: T50025

R:Bevan, M.; Zimmermann, W.; Gruenisen, A.; Wambutt, R.; Kalicki, J.; Wohlmann, P.; S.

Submitted to the Protein Sequence Database, May 2000

A:Reference number: Z25027

A:Accession: T50025

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-197 <BEV>

A:Cross-references: UNIPROT:Q9LX09; EMBL:AL356332; GSPDB:GN00063; ATSP:T31P16.200

A:Experimental source: cultivar Columbia; BAC clone T31P16

C:Genetics:

A:Gene: ATSP:T31P16.200

A:Map position: 5

C:Superfamily: Arabidopsis thaliana hypothetical protein T31P16.200

Query Match 28.6%; Score 58; DB 2; Length 197;

Best Local Similarity 38.5%; Pred. No. 7.1;

Matches 10; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 10 DLDCMDCASCARPHSDFLCGCAA 35

DB 170 DLCECKDRTCNVDYEAFFVACALA 195

Search completed: February 10, 2005, 18:20:12

Job time : 12.2851 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2005, 18:01:53 ; Search time 50.1974 seconds  
(without alignments)  
357.046 Million cell updates/sec

Title: US-10-062-831-59\_COPY\_36\_70

Perfect score: 203  
Sequence: 1 CSRGSSWSADLDKCMDCASCRPHSDFLGCAAA 35

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	203	100.0	129	1 FN14 HUMAN	Q9np84 homo sapien
2	190	93.6	129	1 FN14 MOUSE	Q9cr75 m tumor nec
3	190	93.6	129	2 Q80XJ9	Q80XJ9 rattus norv
4	95	46.8	120	2 Q8SIX7	Q8SIX7 xenopus lae
5	64	31.5	81	1 PORD_METH	P56815 methanobact
6	63.5	31.3	420	2 Q8CBY9	Q8CBY9 mus musculu
7	63.5	31.3	538	2 Q8C278	Q8C278 mus musculu
8	63.5	31.3	681	2 Q8C276	Q8C276 mus musculu
9	63.5	31.3	1005	1 EFA5 RAT	P54757 rattus norv
10	62.5	30.8	1209	2 Q8MIL8	Q8MIL8 sus scrofa
11	61	30.0	56	2 Q7MUS0	Q7MUS0 porphyronon
12	61	30.0	390	2 Q27680	Q27680 methanobact
13	60.5	29.8	76	2 Q24155	Q24155 nicotiana t
14	60.5	29.8	191	2 Q7Q0R6	Q7Q0R6 giardia lam
15	60.5	29.8	495	1 MLP2_DROME	Q24400 drosophila
16	60.5	29.8	1615	2 Q7QZU9	Q7QZU9 giardia lam
17	60	29.6	54	1 FER_PEPAS	P01193 peptostrept
18	59.5	29.3	414	2 Q19088	Q82f5 pyrobaculum
19	59.5	29.3	414	2 Q19088	Q19088 caenorhabdi
20	59.5	29.3	431	1 YG84_METTH	Q27719 methanobact
21	59.5	29.3	645	2 Q86G56	Q26986 homo sapien
22	59.5	29.3	1013	1 EFA5_CHICK	P54755 gallus gall
23	59.5	29.3	1210	1 EGFR_HUMAN	P00533 homo sapien
24	58.5	28.8	328	2 Q76B98	Q76B98 xenopus lae
25	58.5	28.8	396	2 Q7T316	Q7T316 brachydanio
26	58.5	28.8	420	2 P17176	P17176 pacifastacu
27	58.5	28.8	478	2 Q8ESE0	Q8ESE0 rattus norv
28	58.5	28.8	643	2 Q8ERV6	Q8ERV6 mus musculu
29	58.5	28.8	645	2 Q6NPA0	Q6NPA0 drosophila
30	58.5	28.8	655	2 Q9WVF5	Q9WVF5 m epidermal
31	58.5	28.8	751	2 Q9VTR2	Q9VTR2 drosophila

32	58.5	28.8	1210	1 EGFR_MOUSE	Q01279 mus musculu
33	58.5	28.8	1210	2 Q9EP98	Q9EP98 mus musculu
34	58.5	28.8	1877	1 PKC5_MOUSE	Q04592 mus musculu
35	58	28.6	197	2 Q9LX09	Q9LX09 arabidopsis
36	58	28.6	291	2 Q749U7	Q749U7 geobacter s
37	58	28.6	343	2 Q67JAS	Q67JAS symbiobacte
38	58	28.6	789	2 Q8N1E9	Q8N1E9 homo sapien
39	58	28.6	1340	2 Q7PHU6	Q7PHU6 anopheles g
40	58	28.6	1429	2 Q7PBN5	Q7PBN5 anopheles g
41	58	28.6	1433	2 Q9BIH9	Q9BIH9 anopheles g
42	58	28.6	2291	2 Q9WIA9	Q9WIA9 drosophila
43	57.5	28.3	782	2 Q963D5	Q963D5 apis mellif
44	57.5	28.3	1209	2 Q9QX70	Q9QX70 rattus norv
45	57.5	28.3	1696	1 PKC5_BRACL	Q9nj15 branchiosco

#### ALIGNMENTS

RESULT 1  
ID FN14\_HUMAN STANDARD; PRT; 129 AA.  
AC Q9NP84; Q9HCS0;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member Fn14 precursor  
DE (Fibroblast growth factor receptor-inducible immediate-early response protein  
DE 14) (FGF-inducible 14) (Tweak-receptor) (TweakR).  
GN Name=TNFRSF12A; Synonyms=FN14;  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC TISSUE=Placenta;  
RX MEDLINE=20216634; PubMed=10751351;  
RA Peng S.-L.Y., Guo Y., Factor V.M., Thorgeirsson S.S., Bell D.W.,  
RA Testa J.R., Feifley K.A., Winkles J.A.;  
RT "The Fn14 immediate-early response gene is induced during liver  
RT regeneration and highly expressed in both human and murine  
RT hepatocellular carcinomas."  
RL Am J. Pathol. 156:1253-1261(2000).  
[2]  
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
RA Tanaka S., Sugimachi K.;  
RL "Human homologue of Fn14."  
RP Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
[3]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RC TISSUE=Uterus;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[4]  
 FUNCTION.  
 MEDLINE=21585797; PubMed=11728344; DOI=10.1016/S1074-7613(01)00232-1;  
 Wiley S.R., Cassiano L., Lofton T., Davis-Smith T., Winkles J.A.,  
 Lindner V., Liu H., Daniel T.O., Smith C.A., Fanslow W.C.;  
 "A novel TNF receptor family member binds TWEAK and is implicated in  
 angiogenesis";  
 Immunity 15:837-846(2001).  
 CC -!- FUNCTION: Receptor for TNFSF12/TWEAK. Weak inducer of apoptosis in  
 CC some cell types. Promotes angiogenesis and the proliferation of  
 CC endothelial cells. May modulate cellular adhesion to matrix  
 CC proteins.  
 CC -!- SUBUNIT: Associates with TRAF1 and TRAF2, and probably also with  
 CC TRAF3.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=1;  
 CC IsoId=Q9NP84-1; Sequence=Displayed;  
 CC Name=2;  
 CC IsoId=Q9NP84-2; Sequence=VSP\_006519;  
 CC -!- TISSUE SPECIFICITY: Highly expressed in heart, placenta and  
 CC kidney. Intermediate expression in lung, skeletal muscle and  
 CC pancreas.  
 CC -!- INDUCTION: By FGF-1 and phorbol ester.  
 CC -!- SIMILARITY: Contains 1 TNFR-Cys repeat.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 DR EMBL; AF191148; AAF69108.1; -;  
 DR EMBL; AB035480; BAA94792.1; -;  
 DR EMBL; AB035481; BAB17850.1; -;  
 DR EMBL; BC002718; AAB02718.1; -;  
 DR EMBL; HGNC:18152; TNFSF12A.  
 DR H-InvDB; HIX0012751; -;  
 DR MIM; 605914; -;  
 DR GO; GO:0006928; P:cell motility; TAS.  
 DR GO; GO:0007275; P:development; TAS.  
 DR InterPro; IPR001368; TNFR\_c6.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; FALSE NEG.  
 DR PROSITE; PS00050; TNFR\_NGFR\_2; FALSE NEG.  
 KW Alternative splicing; Angiogenesis; Apoptosis; Cell adhesion;  
 KW Receptor; Signal; Transmembrane.  
 FT SIGNAL 1 27 Potential.  
 FT CHAIN 28 129 Tumor necrosis factor receptor  
 FT superfamily member Fn14.  
 FT DOMAIN 28 80 Extracellular (Potential).  
 FT TRANSMEM 81 101 Potential.  
 FT DOMAIN 102 129 Cytoplasmic (Potential).  
 FT REPEAT 36 67 TNFR-Cys (atypical).  
 FT DISULFID 36 49 Potential.  
 FT DISULFID 52 67 Potential.  
 FT VARSPPLIC 33 67 Missing (in isoform 2).  
 FT /FTid=VSP\_006519.  
 SQ SEQUENCE 129 AA; 13911 MW; BF3DFB9C1E1C448 CRC64;  
 Query Match 100.08; Score 203; DB 1; Length 129;  
 Best Local Similarity 100.08; Pred. No. 8e-18;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CSRSSWSADLDKCMDCASCARPHSDFLGCAA 35  
 DQ 36 CSRSSWSADLDKCMDCASCARPHSDFLGCAA 70  
 RESULT 2  
 FN14\_MOUSE

FN14\_MOUSE STANDARD; PRT; 129 AA.  
 Q9CR75; Q9QZW3;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member Fn14 precursor  
 DE (Fibroblast growth factor-inducible immediate-early response protein  
 DE 14) (FGF-inducible 14) (Fibroblast growth factor regulated protein 2)  
 DE (Weak-receptor) (TweakR).  
 DE Name=Tnfrsf12a; Synonyms=Fgfrp2, Fn14;  
 GN Mus musculus (Mouse).  
 OS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC NCBI\_TaxID=10090;  
 OX [1]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=BALB/c; TISSUE=Fibroblast;  
 RC MEDLINE=20020297; PubMed=10551889; DOI=10.1074/jbc.274.46.33166;  
 RX Meighan-Mantha R.L., Hsu D.K.W., Guo Y., Brown S.A.N., Feng S.-L.Y.,  
 RA Peifley K.A., Alberts G.F., Copeland N.G., Gilbert D.J., Jenkins N.A.,  
 RA Richards C.M., Winkles J.A.;  
 RA "The mitogen-inducible Fn14 gene encodes a type I transmembrane  
 RT protein that modulates fibroblast adhesion and migration.";  
 RL J. Biol. Chem. 274:33166-33176(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Placenta;  
 RX MEDLINE=22354681; PubMed=12468851; DOI=10.1038/nature01266;  
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
 RA Nikaide I., Osato R., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
 RA Schiraldi L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
 RA Blake J.A., Bradt D., Brusic V., Chochia C., Corbani L.E., Cousins S.,  
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
 RA McInerney D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,  
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada M.,  
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tonita M.,  
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang L., Yang L.,  
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
 RA Hara A., Haehizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
 RA Yasunishi A., Yoshino M., Waterston K., Lander E.S., Rogers J.,  
 RA Birney E., Hayashizaki Y.;  
 RA "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs";  
 RL Nature 420:563-573(2002).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Breast tumor;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haich P.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.B.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,

```

OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus;
OX NCBI_TaxID=10116;
RP SEQUENCE FROM N.A.
RL Mueller A.M., Giegerich G.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE FROM N.A.
RC TISSUE=Pituitary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.B., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RN SEQUENCE FROM N.A.
RC TISSUE=Pituitary gland;
RA Strausberg R.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY255102; AAP06753.1; -
DR EMBL; BC060537; AAH60537.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR002212; Fibril-assoc.
KW Hypothetical protein; Transmembrane.
SQ SEQUENCE 129 AA; 13616 MW; 57143F979CD7AC77 CRC64;

Query Match 93.6%; Score 190; DB 2; Length 129;
Best Local Similarity 94.3%; Pred. No. 3.4e-16;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0

QY 1 CSRGSSWSADLCKMDCASCARPSPHSDFCILGCAA 35
Db |||||||
36 CSRGSSWSADLCKMDCASCARPSPHSDFCILGCAA 70

RESULT 4
ID Q6SIX7 PRELIMINARY; PRT; 120 AA.
AC Q6SIX7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Fnl4.
GN Name=Fnl4;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA Brown S.A.N., Winkles J.A.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY458020; AAR21225.1; -

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SQ SEQUENCE 120 AA; 13295 MW; F5B5DOBBA3F7B4F CRC64;
Query Match 46.8%; Score 95; DB 2; Length 120;
Best Local Similarity 46.9%; Pred. No. 0.00027;
Matches 15; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

Qy 1 CSRGSSVADLDKMDKDCASCRCARPHSPFLGCG 32
   |||||
Db 27 CPFGAYSQDLGKMCVCKNSKSEKDFCQNC 58

RESULT 5
PORD METHTH STANDARD; PRT; 81 AA.
AC P56815;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Pyruvate synthase subunit pord (EC 1.2.7.1) (Pyruvate oxidoreductase
DE delta chain) (POR) (Pyruvic-ferredoxin oxidoreductase delta subunit).
GN Name=pord; OrderedLocNames=WHI740.1;
OS Methanobacterium thermoautotrophicum.
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
OX NCBI_TaxID=187420;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Delta H;
RX MEDLINE=98037514; PubMed=9371463;
RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
RA Harrison D., Hoang L., Keagle P., Lum W., Pothier B., Qiu D.,
RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
RA Jiwan N., Caruso A., Bush D., Safer H., Patrick D., Prabhakar S.,
RA McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
RA "Complete genome sequence of Methanobacterium thermoautotrophicum
RT deltaH: functional analysis and comparative genomics.";
RL J. Bacteriol. 179:7135-7155(1997).
CC -|- CATALYTIC ACTIVITY: Pyruvate + CoA + oxidized ferredoxin = acetyl-
CC CoA + CO(2) + reduced ferredoxin.
CC -|- COFACTOR: Binds 2 4Fe-4S clusters.
CC -|- SUBUNIT: Heterotetramer of one alpha, one beta, one delta and one
CC gamma chain.
CC -|- SIMILARITY: Contains 2 4Fe-4S type ferredoxin domains.
CC -|- CAUTION: There seems to be a sequencing error that fuses together
CC pord and pord. We have cut the ORF into its two constituents.
-----
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or send an email to license@isb-sib.ch).
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EMBL; AE000929; AAB86210.1; ALT_INIT.
DR HSSP; P00195; ICLF.
DR InterPro; IPR001450; 4Fe4S_ferredoxin.
DR Pfam; PF00037; Fer4; 2.
DR PRINTS; PR00353; 4FE4SFRDOXIN.
DR PROSITE; PS00198; 4FE4S_FERREDOXIN; 2.
KW 4Fe-4S; Complete proteome; Electron transport; Iron-sulfur;
Oxidoreductase; Repeat.
FT METAL 34 34 Iron-sulfur 1 (4Fe-4S) (Potential).
FT METAL 37 37 Iron-sulfur 1 (4Fe-4S) (Potential).
FT METAL 40 40 Iron-sulfur 1 (4Fe-4S) (Potential).
FT METAL 44 44 Iron-sulfur 2 (4Fe-4S) (Potential).
FT METAL 60 60 Iron-sulfur 2 (4Fe-4S) (Potential).
FT METAL 63 63 Iron-sulfur 2 (4Fe-4S) (Potential).
FT METAL 66 66 Iron-sulfur 2 (4Fe-4S) (Potential).
FT METAL 70 70 Iron-sulfur 1 (4Fe-4S) (Potential).
SQ SEQUENCE 81 AA; 9121 MW; 219A9CCAE8A41604 CRC64;
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Query Match 31.5%; Score 64; DB 1; Length 81;
Best Local Similarity 31.9%; Pred. No. 1.4;
Matches 15; Conservative 5; Mismatches 11; Indels 16; Gaps 3;

Qy 2 SRGSSWSA-----DLDKMDKDCASCRA-----RPHS-----DFCLGC 32
   |||||
Db 17 NKTGSWTFKPVLDKDKCIDDCNCLFCPEGCINREHIDVDYCKGC 63
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RESULT 6
Q8CBY9 PRELIMINARY; PRT; 420 AA.
AC Q8CBY9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus adult male diencephalon cDNA, RIKEN full-length enriched
DE library, clone:9330174B07 product:Eph receptor A5, full insert
DE sequence.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Diencephalon;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Diencephalon;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Diencephalon;
RX The FANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Diencephalon;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Diencephalon;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Kono H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Diencephalon;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
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RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,  
RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.,  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AK034289; BAC28660.1; -  
DR HSSP; P54763; 1NUK.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0005003; F:ephrin receptor activity; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.  
DR InterPro; IPR006209; EGF like.  
DR InterPro; IPR001090; Ephrin receptor.  
DR InterPro; IPR008979; Gal bind like.  
DR InterPro; IPR009030; Grow\_fac\_recept.  
DR InterPro; IPR001426; Ykase\_receptor.  
DR Pfam; PF01404; Ephrin\_lbd; 1.  
DR ProDom; PD001495; Ephrin\_receptor; 1.  
DR SMART; SM00615; EPH\_lbd; 1.  
DR PROSITE; PS01186; EGF\_2; 1.  
DR PROSITE; PS00790; RECEPTOR\_TYR\_KIN\_V\_1; 1.  
DR PROSITE; PS00791; RECEPTOR\_TYR\_KIN\_V\_2; 1.  
KW Receptor.  
SQ SEQUENCE 420 AA; 46434 MW; 8860ADE8F73C98D4 CRC64;  
Query Match 31.3%; Score 63.5; DB 2; Length 420;  
Best Local Similarity 31.9%; Pred.No. 7.5;  
Matches 15; Conservative 1; Mismatches 16; Indels 15; Gaps 2;  
QY 1 CSRSWSADLDKCM-----DCASCR-----ARPHSDFCLGC 32  
DB 278 CSAEGLVPIQCKMCKAGYEKNGTCQCRPFKASPHSQTCSKC 324  
RESULT 7  
Q8C278 PRELIMINARY; PRT; 538 AA.  
ID Q8C278;  
AC Q8C278;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Mus musculus 10 days neonate olfactory brain cDNA, RIKEN full-length  
DE enriched library, clone:E530011F10 product:Eph receptor A5, full  
DE insert sequence.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]\_TaxID=10090;  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;  
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
RA Carninci P., Hayashizaki Y.;  
RT "High-efficiency full-length cDNA cloning.";  
RL Meth. Enzymol. 303:19-44(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;  
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
RA RIKEN FANTOM Consortium;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;

RA The FANTOM Consortium,  
RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs.";  
RL Nature 420:563-573(2002).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;  
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
RL Genome Res. 10:1617-1630(2000).  
RN [5]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;  
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
RA Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,  
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
RA Yanamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
RT "RIKEN integrated sequence analysis (RISA) system-384-format  
RT sequencing pipeline with 384 multicapillary sequencer.";  
RL Genome Res. 10:1757-1771(2000).  
RN [6]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;  
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,  
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,  
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.,  
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AK089130; BAC40761.1; -  
DR HSSP; P54763; 1NUK.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0005003; F:ephrin receptor activity; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.  
DR InterPro; IPR006209; EGF like.  
DR InterPro; IPR001090; Ephrin\_receptor.  
DR InterPro; IPR003962; FNIII\_subd.  
DR InterPro; IPR003961; FN\_III.  
DR InterPro; IPR008957; FN\_III-like.  
DR InterPro; IPR008979; Gal bind like.  
DR InterPro; IPR009030; Grow\_fac\_recept.  
DR InterPro; IPR001426; Ykase\_receptor.  
DR Pfam; PF01404; Ephrin\_lbd; 1.  
DR Pfam; PF00041; fn3; 1.  
DR PRINTS; PR00014; FNTYPEIII.  
DR ProDom; PD001495; Ephrin\_receptor; 1.  
DR SMART; SM00615; EPH\_lbd; 1.  
DR SMART; SM00060; FN3; 1.  
DR PROSITE; PS01186; EGF\_2; 1.  
DR PROSITE; PS00853; FN3; 1.  
DR PROSITE; PS00790; RECEPTOR\_TYR\_KIN\_V\_1; 1.  
DR PROSITE; PS00791; RECEPTOR\_TYR\_KIN\_V\_2; 1.  
KW Receptor.  
SQ SEQUENCE 538 AA; 59823 MW; CF48C4F981452515 CRC64;  
Query Match 31.3%; Score 63.5; DB 2; Length 538;





RA Taylor V., Miescher G.C., Pfarr S., Honegger P., Breitschopf H.,  
 RA Lasemann H., Steck A.J.;  
 RT "Expression and developmental regulation of EphA-1, a neuronal Elk-like  
 RT receptor tyrosine kinase in brain.";  
 RL Neuroscience 63:163-178 (1994)  
 CC -!- FUNCTION: Receptor for members of the ephrin-A family. Binds to  
 CC ephrin-A1, -A2, -A3, -A4 and -A5.  
 CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
 CC tyrosine phosphate.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event-Alternative splicing; Named isoforms=6;  
 CC Name=1;  
 CC IsoId=P54757-1; Sequence=Displayed;  
 CC Name=2;  
 CC IsoId=P54757-2; Sequence=VSP\_003001;  
 CC Name=3;  
 CC IsoId=P54757-3; Sequence=VSP\_003002;  
 CC Name=4;  
 CC IsoId=P54757-4; Sequence=VSP\_003002, VSP\_003003;  
 CC Name=5;  
 CC IsoId=P54757-5; Sequence=VSP\_003001, VSP\_003002, VSP\_003003;  
 CC Name=6;  
 CC IsoId=P54757-6; Sequence=VSP\_003000, VSP\_003002;  
 CC -!- TISSUE SPECIFICITY: Almost exclusively expressed in the nervous  
 CC system. Predominantly expressed in neurons.  
 CC -!- SIMILARITY: Belongs to the Tyr protein kinase family. Ephrin  
 CC receptor subfamily.  
 CC -!- SIMILARITY: Contains 2 fibronectin type III domains.  
 CC -!- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC -----  
 DR EMBL; X78589; CAA55357.1; -;  
 DR PIR; S49015; S49015;  
 DR PIR; S51603; S51603;  
 DR HSSP; P54763; 1JFA.  
 DR InterPro; IPR006209; EGF like.  
 DR InterPro; IPR001090; Ephrin receptor.  
 DR InterPro; IPR003961; FN III-  
 DR InterPro; IPR008957; FN III-like.  
 DR InterPro; IPR003962; FNIII\_subd.  
 DR InterPro; IPR008979; Gal\_bind\_like.  
 DR InterPro; IPR009030; Grow\_fac\_recept.  
 DR InterPro; IPR011009; Kinase like.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR001660; SAM.  
 DR InterPro; IPR001245; Tyr\_kinase.  
 DR InterPro; IPR008266; Tyr\_kinase\_AS.  
 DR InterPro; IPR001426; Ykase\_receptorV.  
 DR Pfam; PF01404; Ephrin\_lbd; 1.  
 DR Pfam; PF00041; fn3\_2  
 DR Pfam; PF00069; Pkinase; 1.  
 DR Pfam; PF00536; SAM; 1.  
 DR PRINTS; PR00014; FNTYPEIII.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR ProDom; PD001495; Ephrin\_receptor; 1.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00615; EPH\_lbd; 1.  
 DR SMART; SM00060; FN3; 2.  
 DR SMART; SM00219; TyrKc; 1.  
 DR PROSITE; PS01186; EGF\_2;  
 DR PROSITE; PS00853; FN3; 2.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; FALSE\_NEG.  
 DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE; PS00790; RECEPTOR\_TYR\_KIN\_V\_1; 1.

DR PROSITE; PS00791; RECEPTOR\_TYR\_KIN\_V\_2; 1.  
 KW ALTERNATIVE SPLICING; ATP-binding; Glycoprotein; Phosphorylation;  
 KW Receptor; Repeat; Signal; Transmembrane;  
 KW Tyrosine-protein kinase.  
 FT SIGNAL 1 26 By similarity.  
 FT CHAIN 27 1005 Ephrin type-A receptor 5.  
 FT DOMAIN 27 575 Extracellular (Potential).  
 FT TRANSMEM 576 596 Potential.  
 FT DOMAIN 597 1005 Cytosolic (Potential).  
 FT DOMAIN 222 356 Cys-rich.  
 FT DOMAIN 359 461 Fibronectin type-III 1.  
 FT DOMAIN 471 561 Fibronectin type-III 2.  
 FT DOMAIN 677 938 Protein kinase.  
 FT DOMAIN 967 1005 SAM.  
 FT NP\_BIND 683 691 ATP (By similarity).  
 FT BINDING 709 709 ATP (By similarity).  
 FT ACT\_SITE 802 802 Phosphotyrosine (by autocatalysis) (By  
 FT MOD\_RES 652 652 similarity).  
 FT MOD\_RES 658 658 Phosphotyrosine (by autocatalysis) (By  
 FT MOD\_RES 835 835 similarity).  
 FT MOD\_RES 984 984 Phosphotyrosine (by autocatalysis) (By  
 FT CARBOHYD 266 266 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 301 301 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 371 371 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 425 425 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 438 438 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 463 463 N-linked (GlcNAc...) (Potential).  
 FT VARSPPLIC 10 20 GRRTOGRGGG -> DADGPRQAQSMCHARR (in  
 FT isoform 6).  
 FT VARSPPLIC 306 357 /FTId=VSP\_003000.  
 FT VARSPPLIC 358 470 VCRPGFFKASPHQTCCKCPHPSYTHEASVSCVCEKDYFR  
 FT RESDPTMACT -> G (in isoform 2 and  
 FT isoform 5).  
 FT VARSPPLIC 358 470 /FTId=VSP\_003001.  
 FT RPPSPAPRNAINVNETSVFLEWIPADTGGGKQVSYIILCK  
 FT KNSHAGVCGSGGHRVLPQOIGKNTSVMMADPLAHNTY  
 FT TFEIEAVNGVSDLSFGTRQYVNVNTNQA -> T (in  
 FT isoform 3, isoform 4, isoform 5 and  
 FT isoform 6).  
 FT VARSPPLIC 597 621 /FTId=VSP\_003002.  
 FT SGSCCEGCGRASSLCVAHPSLIW -> R (in  
 FT isoform 4 and isoform 5).  
 FT CONFLICT 170 170 D -> E (in Ref. 2).  
 FT CONFLICT 566 566 G -> A (in Ref. 2).  
 FT CONFLICT 578 578 G -> A (in Ref. 2).  
 FT CONFLICT 669 669 G -> A (in Ref. 2).  
 FT CONFLICT 708 708 T -> I (in Ref. 2).  
 FT CONFLICT 979 979 T -> I (in Ref. 2).  
 SQ SEQUENCE 1005 AA; 111007 MW; 1AED42C99693C574 CRC64;  
 Query Match 31.3%; Score 63.5; DB 1; Length 1005;  
 Best Local Similarity 31.9%; Pred. No. 17;  
 Matches 15; Conservative 1; Mismatches 16; Indels 15; Gaps 2;  
 Oy 1 CSRGSSWSADLCKM-----DCASCR-----ARPHSDFCLGC 32  
 ||| : |||  
 Db 278 CSARGEMLVPIGKCMCKAGYEKNGTCQVCRPGFFKASPHSQTCCK 324  
 ||| : |||  
 RESULT 10;  
 Q8MIL8  
 ID Q8MIL8 PRELIMINARY; .PRT; 1209 AA.  
 AC Q8MIL8;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Epidermal growth factor receptor.

OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Kim J.G., Vallet J.L., Nonneman D., Christenson R.K.;  
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY117054; AAM77472.1; -  
DR HSSP; Q9H2C9; 1M17.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0005006; F:epidermal growth factor receptor activity; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0016740; F:transferase activity; IEA.  
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
DR GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. .; IEA.  
DR InterPro; IPR000345; CyC heme\_BS.  
DR InterPro; IPR000494; EGFR\_L.  
DR InterPro; IPR006211; Furin-like.  
DR InterPro; IPR006212; Furin repeat.  
DR InterPro; IPR009030; Grow fac recept.  
DR InterPro; IPR011009; Kinase like.  
DR InterPro; IPR000719; Prot kinase.  
DR InterPro; IPR001245; Tyr\_kinase.  
DR InterPro; IPR008266; Tyr\_kinase\_AS.  
DR Pfam; PF00757; Furin-like; 1.  
DR PRINTS; PF01030; Recep\_L domain; 2.  
DR PRINTS; PR00109; TYRKINASE.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR SMART; SM00261; FU; 5.  
DR SMART; SM00219; TyRKC; 1.  
DR PROSITE; PS00190; CYTOCHROME\_C; UNKNOWN 1.  
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.  
DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
KW ATP-binding; Kinase; Receptor; Transferase; Tyrosine-protein kinase.  
SQ SEQUENCE 1209 AA; 133531 MW; 268E3P11E36F90F CRC64;

Query Match 30.8%; Score 62.5; DB 2; Length 1209;  
Best Local Similarity 37.8%; Pred. No. 27;  
Matches 17; Conservative 1; Mismatches 16; Indels 11; Gaps 3;

Qy 1 CSRGSSWADLDKMD-----CAS-----CRAPHSDFCLG-CAA 34  
Db 194 CLNGSCWAGXGKNCOKLTKVICAQCRCGRSPSCCHNQCAA 238

RESULT 11  
Q7MUS0 PRELIMINARY; PRT; 56 AA.  
ID Q7MUS0  
AC Q7MUS0  
DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Periredoxin, 4Fe-4S  
GN OrderedLocNames=PGI421;  
OS Porphyromonas gingivalis (Bacteroides gingivalis).  
OC Bacteria; Bacteroidetes; Bacteroides (Class); Bacteroidales;  
OC Porphyromonadaceae; Porphyromonas.  
OX NCBI\_TaxID=837;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=W83;  
RX MEDLINE=22829867; PubMed=12949112;  
RX DOI=10.1128/JB.185.18.5591-5601.2003;  
RA Nelson K.E., Fleischmann R.D., DeBoy R.T., Paulsen I.T., Fouts D.E.,  
RA Eisen J.A., Daugherty S.C., Dodson R.J., Durkin A.S., Gwinn M.L.,  
RA Haft D.H., Kolonay J.F., Nelson W.C., Mason T.M., Tallon L., Gray J.,  
RA Granger D., Tettelin H., Dong H., Galvin J.L., Duncan M.J.,  
RA Dewhirst F.E., Fraser C.M.;  
RT "Complete genome sequence of the oral pathogenic bacterium  
Porphyromonas gingivalis strain W83.";

RL J. Bacteriol. 185:5591-5601(2003).  
DR EMBL; AE017176; AAQ66475.1; -  
DR HSSP; P00195; ICLF.  
DR TIGR; PGI421; -  
DR GO; GO:0005489; F:electron transporter activity; IEA.  
DR GO; GO:0005506; F:iron ion binding; IEA.  
DR GO; GO:0006118; F:electron transport; IEA.  
DR InterPro; IPR001450; 4Fe4S ferredoxin.  
DR InterPro; IPR000813; 7Fe ferredoxin.  
DR Pfam; PF00037; Fer4; 2.  
DR PRINTS; PR00353; 4FE4SFRDOXIN.  
DR PRINTS; PR00354; 7FE8SFRDOXIN.  
DR PROSITE; PS00198; 4FE4S FERREDOXIN; 2.  
KW 4Fe-4S; Complete proteome; Iron; Iron-sulfur; Metal-binding.  
SQ SEQUENCE 56 AA; 5688 MW; 571153F92BB10C57 CRC64;

Query Match 30.0%; Score 61; DB 2; Length 56;  
Best Local Similarity 47.6%; Pred. No. 2.4;  
Matches 10; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

Qy 2 SRGSSWADLDKMDCASCEA 22  
Db 25 SEGSYKIDATCTIDCGTCAA 45

RESULT 12  
O27680 PRELIMINARY; PRT; 390 AA.  
ID O27680  
AC O27680  
DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Pyruvate formate-lyase activating enzyme related protein.  
GN OrderedLocNames=WH1643;  
OS Methanobacterium thermoautotrophicum.  
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;  
OC Methanobacteriaceae; Methanothermobacter.  
OX NCBI\_TaxID=187420;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Delta H;  
RX MEDLINE=98037514; PubMed=9371463;  
RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,  
RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,  
RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,  
RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,  
RA Jiwanji N., Caruso A., Bush D., Safer H., Batwell D., Prabhakar S.,  
RA McDougall S., Shimer G., Goyal A., Pietrowski S., Church G.M.,  
RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;  
RT "Complete genome sequence of Methanobacterium thermoautotrophicum  
deltaH; functional analysis and comparative genomics.";  
RL J. Bacteriol. 179:7135-7155(1997).  
DR EMBL; AE000923; AAB86116.1; -  
DR PIR; F69086; F69086.  
DR GO; GO:0005489; F:electron transporter activity; IEA.  
DR GO; GO:0005506; F:iron ion binding; IEA.  
DR GO; GO:0016829; F:lyase activity; IEA.  
DR GO; GO:0006118; F:electron transport; IEA.  
DR InterPro; IPR001450; 4Fe4S ferredoxin.  
DR InterPro; IPR006638; Elp3/Miab/NifB.  
DR InterPro; IPR001041; Ferredoxin.  
DR InterPro; IPR007197; Radical SAM.  
DR Pfam; PF00037; Fer4; 1.  
DR Pfam; PF04055; Radical SAM; 1.  
DR PRINTS; PR00353; 4FE4SFRDOXIN.  
DR SMART; SM00729; Elp3; 1.  
KW PROSITE; PS00198; 4FE4S FERREDOXIN; 1.  
KW 4Fe-4S; Complete proteome; Iron; Iron-sulfur; Lyase; Metal-binding;  
PYruvate.  
SQ SEQUENCE 390 AA; 42559 MW; B1F207E290AD52FC CRC64;

Query Match 30.0%; Score 61; DB 2; Length 390;  
Best Local Similarity 43.5%; Pred. No. 14;

Matches 10; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 12 DKMDASCARPHSDFCIGCAA 34  
 Db 14 DRCGCGNCKSENCTGCA 36

RESULT 13  
 Q24155 PRELIMINARY; PRT; 76 AA.  
 AC Q24155  
 DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE TA20 protein.  
 GN Name=TA20;  
 OS Nicotiana tabacum (Common tobacco).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
 OC Lamiales; Solanales; Solanaceae; Nicotiana.  
 OX NCBI\_TaxID=4097;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Anther;  
 RA Beals T.P., Goldberg R.B.;  
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U73164; AAB18190.1; -;  
 DR PIR; T03860; T03860.  
 DR InterPro; IPR001212; Somatomedin\_B.  
 DR PRINTS; PR00022; SOMATOMEDINB.  
 SQ SEQUENCE 76 AA; 8269 MW; 2F0A47BF7A52F7CC CRC64;

Query Match 29.8%; Score 60.5; DB 2; Length 76;  
 Best Local Similarity 40.0%; Pred. No. 3.7;  
 Matches 12; Conservative 4; Mismatches 9; Indels 5; Gaps 1;

QY 5 SWSADLDKCMD-----CASCARPHSDFC 29  
 Db 27 SSYAADGSDCTDHCAITCAFCNGKQYNVC 56

RESULT 14  
 Q7QOR6 PRELIMINARY; PRT; 191 AA.  
 AC Q7QOR6  
 DT 01-MAR-2004 (TREMBLrel. 26, Created)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE GLP 24.24180.23605.  
 OS Giardia lamblia ATCC 50803.  
 OC Eukaryota; Diplomonadida; Hexamitidae; Giardia.  
 OX NCBI\_TaxID=184922;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=WB C6;  
 RA Morrison H.G.;  
 RA Olsen G.J., Sogin M.L.;  
 RT "Draft sequence of the Giardia lamblia genome."  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
 CC -!- CAUTION: The sequence shown here is derived from an  
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 preliminary data.  
 CC EMBL; AACB01000143; EAA37372.1; -;  
 DR HSSP; P01180; 1JK6.  
 DR InterPro; IPR006058; 2Fe2S\_fd\_BS.  
 DR InterPro; IPR009030; Grow\_fac\_recpt.  
 DR PROSITE; PS00197; 2FE2S\_FERREDOXIN; UNKNOWN 1.  
 SQ SEQUENCE 191 AA; 18964 MW; 8F52AED18A477E5B CRC64;

Query Match 29.8%; Score 60.5; DB 2; Length 191;  
 Best Local Similarity 41.2%; Pred. No. 8.7;  
 Matches 14; Conservative 3; Mismatches 14; Indels 3; Gaps 2;

QY 1 CSRGSSWADLDKCMDAS-CRARPHSDFCIGCA 33  
 Db 46 CKRG--WHLAGDCLACSPCAACSSAASCLACA 77

RESULT 15  
 MLP2 DROME  
 ID MLP2 DROME STANDARD; PRT; 495 AA.  
 AC Q24400; Q3VI62;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 25-JAN-2005 (Rel. 46, Last annotation update)  
 DE Muscle LIM protein Mlp84B.  
 GN Name=Mlp84B; Synonyms=LIM3; ORFNames=CG10699;  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.; FUNCTION, SUBCELLULAR LOCATION, TISSUE  
 SPECIFICITY, AND DEVELOPMENTAL STAGE.  
 RX MEDLINE=96387325; PubMed=8794860; DOI=10.1083/jcb.134.5.1179;  
 RA Stronach B.E., Siegrist S.E., Beckerle M.C.;  
 RT "Two muscle-specific LIM proteins in Drosophila.";  
 RL J. Cell Biol. 134:1179-1195(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.; FUNCTION, AND TISSUE SPECIFICITY.  
 RX MEDLINE=99328429; PubMed=10397768;  
 RA Stronach B.E., Renfranz P.J., Lilly B., Beckerle M.C.;  
 RT "Muscle LIM proteins are associated with muscle sarcomeres and require  
 DMEF2 for their expression during Drosophila myogenesis.";  
 RL Mol. Biol. Cell 10:2329-2342(1999).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkley;  
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazer E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W.,  
 RA Foster C., Gabrielian A.B., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasoko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,  
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;



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# OM protein - protein search, using sw model

Run on: February 10, 2005, 17:53:53 ; Search time 55.5702 Seconds  
(without alignments)  
243.595 Million cell updates/sec

Title: us-10-062-831-59\_COPY\_36\_70

Perfect score: 203

Sequence: 1 CSRGSSWSADLKDCKDCASCARPHSDFLGCAAA 35

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

- 1: Geneseqp1980a:\*
- 2: Geneseqp1990a:\*
- 3: Geneseqp2000a:\*
- 4: Geneseqp2001a:\*
- 5: Geneseqp2002a:\*
- 6: Geneseqp2003a:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004a:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	203	100.0	114	2	AAW73409 Human sec
2	203	100.0	129	2	AAW88506 Human liv
3	203	100.0	129	3	AAV57940 Human tra
4	203	100.0	129	4	AAU03498 Human TWE
5	203	100.0	129	5	ABP61512 Human NP-
6	203	100.0	129	5	AAU79827 Human typ
7	203	100.0	129	6	ADA56889 Human sec
8	203	100.0	129	6	ADU56716 Lung carc
9	203	100.0	129	7	ADG74112 Human sec
10	203	100.0	129	7	ADG37867 Human sec
11	203	100.0	129	7	ADD89033 TAT274.1
12	203	100.0	129	7	ABU64232 Human FRA
13	203	100.0	129	7	ADN39126 Cancer/an
14	203	100.0	129	7	ADN39987 Cancer/an
15	203	100.0	129	8	ABM81706 Tumour-as
16	203	100.0	309	4	AAU03500 Human TWE
17	191	94.1	32	6	ADA49370 Human Fnl
18	190	93.6	129	5	AAU79828 Mouse typ
19	104.5	51.5	112	3	AAV91463 Human sec
20	104.5	51.5	112	6	ADA57390 Human sec
21	104.5	51.5	112	7	ADC74462 Human sec
22	104.5	51.5	112	7	ADD38025 Human sec
23	104.5	51.5	112	8	ADL71535 Novel hum
24	104.5	51.5	155	3	AAV91604 Human sec
25	104.5	51.5	155	6	ADA57391 Human sec

26	104.5	51.5	155	7	ADC74463 Human sec
27	104.5	51.5	155	7	ADD38026 Human sec
28	104.5	51.5	155	8	ADL71680 Novel hum
29	104.5	51.5	156	3	AAV91552 Human sec
30	104.5	51.5	156	8	ADL71624 Novel hum
31	68	33.5	248	7	ABO80503 Pseudomon
32	65	32.0	400	7	ABO77399 Pseudomon
33	64	31.5	974	7	AAE38808 Human POL
34	63.5	31.3	928	2	AAE97853 Rat REK7
35	63.5	31.3	1005	2	AAW83147 Rat recep
36	60.5	29.8	495	4	ABB57748 Drosophil
37	60.5	29.8	495	4	ABB57752 Drosophil
38	60	29.6	403	6	ABU52378 Human GPC
39	60	29.6	403	8	ADL24091 Human NOV
40	60	29.6	1188	8	ADO28625 Human EGF
41	59.5	29.3	405	2	AAW33737 Epidermal
42	59.5	29.3	405	5	AAE23001 Human Her
43	59.5	29.3	405	7	ADD25482 Binding d
44	59.5	29.3	405	7	ADD25488 Binding d
45	59.5	29.3	405	8	ADR24015 Human epi

## ALIGNMENTS

RESULT 1  
AAW73409  
ID AAW73409 standard; protein; 114 AA.  
XX  
AC AAW73409;  
XX  
DT 19-FEB-1999 (first entry)  
XX  
DE Human secreted protein encoded by Gene No. 13.  
XX  
KW Secreted protein; human; protein therapy; gene therapy; blood disorder;  
KW pathological condition; diagnosis; cancer; neurological disorder;  
KW developmental abnormality; fetal deficiency; leukaemia; hepatic disease;  
KW immune system disorder; Alzheimer's disease; cognitive disorder;  
KW schizophrenia; prostate disease; autoimmune disorder; AIDS.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 114  
FT /note= "unspecified amino acid"  
XX  
PN WO9854206-A1.  
XX  
PD 03-DEC-1998.  
XX  
PF 28-MAY-1998; 98WO-US010868.  
XX  
PR 30-MAY-1997; 97US-0044039P.  
PR 30-MAY-1997; 97US-0048093P.  
PR 30-MAY-1997; 97US-0048101P.  
PR 30-MAY-1997; 97US-0048190P.  
PR 30-MAY-1997; 97US-0048356P.  
PR 30-MAY-1997; 97US-0050935P.  
PR 29-AUG-1997; 97US-0056250P.  
PR 29-AUG-1997; 97US-0056293P.  
PR 29-AUG-1997; 97US-0056296P.  
XX  
(HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM, Rosen CA, Carter KC, Dillon PJ, Endress GA, Yu G;  
PI Ni J, Feng F;  
XX WPI; 1999-070209/06.  
DR N-PSDB; AAV08823.  
XX  
PT New isolated human genes - useful for diagnosis and treatment of, e.g.  
PT cancers, neurological disorders, immune diseases, developmental disorders

PT or blood disorders.

PS Claim 11; Page 153; 18pp; English.

XX This sequence is encoded by a cDNA of the invention, designated Gene No. 13. This sequence represents a human secreted protein, and is expressed in keratinocytes and to a lesser extent in endothelial cells and placenta. The DNA sequences of the invention and their corresponding secreted polypeptides are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the DNA sequences. Specific uses are described for each of the DNA sequences and the encoded proteins, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, neurological disorders, developmental abnormalities and foetal deficiencies, blood disorders, leukaemias, diseases of the immune system (including allergies or asthma), hepatic disease, Alzheimer's and cognitive disorders, schizophrenia, prostate disease, autoimmune disorders and AIDS. The polypeptides are also useful for identifying their binding partners

XX Sequence 114 AA;

Query Match 100.0%; Score 203; DB 2; Length 114;

Best Local Similarity 100.0%; Pred. No. 1.2e-16;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSRGSSWSADLDKCMDCASCARPHSDFCIGCAA 35  
|||||

Db 36 CSRGSSWSADLDKCMDCASCARPHSDFCIGCAA 70  
|||||

RESULT 2

AAW88506

ID AAW88506 standard; protein; 129 AA.

AC AAW88506;

XX

XX 30-MAR-1999 (first entry)

DE Human liver clone HP10432-encoded membrane protein.

XX Transmembrane protein; HP10432; human; liver.

XX

XX Homo sapiens.

XX WO9855508-A2.

XX 10-DEC-1998.

XX

XX 03-JUN-1998; 98WO-JP002445.

XX

XX 03-JUN-1997; 97JP-00144948.

XX (SAGA) SAGAMI CHEM RES CENTRE.

PA (PROT-) PROTEGENE INC.

XX Kato S, Sekine S, Yamaguchi T;

XX WPI; 1999-045730/04.

DR N-PSDB; AAW84374.

XX

XX New human proteins containing transmembrane domains and their encoding sequences - useful in the preparation of antibodies and large-scale protein production, gene diagnosis, and gene therapy.

XX Claim 1; Page 152-153; 178pp; English.

XX This is the amino acid sequence of a transmembrane protein encoded by human liver cDNA clone HP10432 (see AAW84374). The encoded protein has a signal-like N-terminal region and one internal transmembrane domain. The invention provides nucleotide sequences (see AAW84359-76) coding for 18

CC transmembrane proteins (see AAW88491-508), vectors containing such polynucleotides, and eukaryotic cells containing the vectors. The proteins can be used as antigens or as compositions in the preparation of antibodies against the proteins. The polynucleotides can be used as probes for gene diagnosis, and as gene sources for gene therapy and large-scale production of proteins encoded by the cDNA. The host cells are used for the detection of ligands corresponding to the expressed proteins, and the screening of low mol.wt. medicines

XX Sequence 129 AA;

Query Match 100.0%; Score 203; DB 2; Length 129;

Best Local Similarity 100.0%; Pred. No. 1.4e-16;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSRGSSWSADLDKCMDCASCARPHSDFCIGCAA 35  
|||||

Db 36 CSRGSSWSADLDKCMDCASCARPHSDFCIGCAA 70  
|||||

RESULT 3

AAW57940

ID AAW57940 standard; protein; 129 AA.

XX

XX AAW57940;

XX

XX 23-MAR-2000 (first entry)

DE Human transmembrane protein HTMPN-64.

XX

XX Human; transmembrane protein; HTMPN; diagnosis; immunospecific; antiproliferative; neuroprotective; immune disorder;

KW reproductive disorder; smooth muscle disorder; neurological disorder;

KW gastrointestinal disorder; developmental disorder;

KW cell proliferative disorder.

XX

XX Homo sapiens.

XX WO9961471-A2.

XX

XX 02-DEC-1999.

XX

XX 28-MAY-1999; 99WO-US011904.

XX

XX 29-MAY-1998; 98US-0087260P.

PR 02-JUL-1998; 98US-0091674P.

PR 02-OCT-1998; 98US-0102954P.

PR 24-NOV-1998; 98US-0109869P.

XX

XX (INCY-) INCYTE PHARM INC.

XX Tang YT, Lal P, Hillman JL, Yue H, Guegler KJ, Corley NC;

PI Bandman O, Patterson C, Gorgone GA, Kasser MR, Baughn MR, Au-Young J;

XX

XX WPI; 2000-072605/06.

DR N-PSDB; AAW56761.

XX

XX Proteins, polynucleotides, vectors, host cells and antibodies used to diagnose, treat or prevent immune, reproductive, smooth muscle, neurological, gastrointestinal, developmental and cell proliferative disorders.

PT

PT disorders.

XX

XX Claim 1; Page 163; 229pp; English.

XX AAW56698 to AAW56776 encode AAW57877 to AAW57955 which represent human transmembrane proteins designated HTMPN-1 to HTMPN-79, respectively. The transmembrane protein have immunospecific, antiproliferative and neuroprotective activities. The human transmembrane proteins, polynucleotides encoding them and other compositions and methods from the present invention, can be used for the diagnosis, treatment or prevention of immune, reproductive, smooth muscle, neurological, gastrointestinal, developmental and cell proliferative disorders. The HTMPN's can be used to treat or prevent disorders associated with a decreased expression or

CC activity of HTMPN  
 XX Sequence 129 AA;  
 SQ Query Match 100.0%; Score 203; DB 3; Length 129;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-16;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSRGSSWSADLDKCMDCASCARPHSDFCGLGCAA 35  
 DB 36 CSRGSSWSADLDKCMDCASCARPHSDFCGLGCAA 70

RESULT 4  
 ID AAU03498 standard; protein; 129 AA.  
 AC AAU03498;  
 XX 26-SEP-2001 (first entry)  
 XX Human TWEAK receptor (TWEAKR) polypeptide.

DE TWEAK receptor; TWEAKR; tumour necrosis factor; TNF; angiogenesis;  
 KW ocular neovascularisation; diabetic retinopathy; neovascular glaucoma;  
 KW retinoblastoma; retinopathy of prematurity; retrolental fibroplasia;  
 KW rubecosis; uveitis; macular degeneration; arthritis; rheumatism;  
 KW corneal graft neovascularisation; psoriasis; metastatic condition;  
 KW malignant tumour; sarcoma; carcinoma; benign tumour; haemophilic joint;  
 KW preneoplastic condition; myocardial angiogenesis; wound granulation;  
 KW scleroderma; vascular adhesion; telangiectasia; ischaemia; human;  
 KW atherosclerotic plaque neovascularisation; coronary atherosclerosis;  
 KW peripheral atherosclerosis.  
 XX Homo sapiens.

OS Key Location/Qualifiers  
 FH Domain 1..78  
 FT /note= "Extracellular domain"  
 FT Peptide 1..27  
 FT /note= "Signal peptide"  
 FT Protein 28..129  
 FT /note= "Mature human TWEAKR protein"  
 FT Domain 79..101  
 FT /note= "Transmembrane domain"  
 FT Domain 102..129  
 FT /note= "Intracellular domain"

XX WO200145730-A2.  
 XX 28-JUN-2001.  
 XX 19-DEC-2000; 2000WO-US034755.  
 XX 20-DEC-1999; 99US-0172878P.  
 XX 10-MAY-2000; 2000US-0203347P.  
 XX (IMMV) IMMUNEX CORP.  
 XX Wiley SR;  
 XX WPI; 2001-417975/44.  
 XX N-PSDB; AAS03963.  
 XX Modulating angiogenesis in a mammal for treating diseases mediated by  
 PT angiogenesis, e.g. solid tumors and vascular deficiencies of cardiac or  
 PT peripheral tissue, by administering antagonist or agonist of TWEAK  
 PT receptor.  
 XX Example 1; Fig 1; 46pp; English.  
 XX The sequence represents the human TWEAK receptor (TWEAKR) protein. The  
 CC TWEAK protein is a member of the tumour necrosis factor (TNF) family and

CC induces angiogenesis. TWEAKR may therefore be used to screen for and  
 CC develop TWEAKR agonists and antagonists for the modulation of  
 CC angiogenesis, to be used in the treatment and diagnosis of human disease.  
 CC The disorders mediated by angiogenesis include ocular disorders  
 CC characterised by ocular neovascularisation such as diabetic retinopathy,  
 CC neovascular glaucoma, retinoblastoma, retinopathy of prematurity, and  
 CC retrolental fibroplasia, rubecosis, uveitis, macular degeneration and  
 CC corneal graft neovascularisation, and inflammatory diseases such as  
 CC arthritis, rheumatism and psoriasis. Other treatable diseases include  
 CC malignant and metastatic conditions such as sarcomas and carcinomas,  
 CC benign tumours and preneoplastic conditions, myocardial angiogenesis,  
 CC haemophilic joints, scleroderma, vascular adhesions, atherosclerotic  
 CC plaque neovascularisation, telangiectasia, wound granulation, coronary  
 CC atherosclerosis, peripheral atherosclerosis and ischaemia  
 XX Sequence 129 AA;  
 SQ Query Match 100.0%; Score 203; DB 4; Length 129;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-16;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSRGSSWSADLDKCMDCASCARPHSDFCGLGCAA 35  
 DB 36 CSRGSSWSADLDKCMDCASCARPHSDFCGLGCAA 70

RESULT 5  
 ABP61512  
 ID ABP61512 standard; protein; 129 AA.  
 XX ABP61512;  
 XX 30-SEP-2002 (first entry)  
 XX Human NF-kB activating protein SEQ ID NO 178.

DE Human; NF-kB; nuclear factor kappa B; mouse; antiinflammatory;  
 KW immunomodulator; cytostatic; antiinfective; osteopathic; nootropic;  
 KW neuroprotective; anti-HIV; autoimmune disease; cancer; infection;  
 KW bone disease; AIDS; neurodegenerative disease; ischaemic disorder.  
 XX Homo sapiens.  
 OS WO200253737-A1.  
 XX 11-JUL-2002.  
 XX 25-DEC-2001; 2001WO-JP011389.  
 XX 28-DEC-2000; 2000JP-00402288.  
 XX 26-MAR-2001; 2001JP-00088912.  
 XX 24-AUG-2001; 2001JP-00254018.  
 XX (ASAH) ASAH KASEI KOGYO KK.  
 XX Matsuda A, Honda G, Muramatsu S, Nagano Y;  
 DR WPI; 2002-583617/62.  
 DR N-PSDB; ABQ92000.  
 XX NF-approximatelykB activating gene and expressed protein, applicable in  
 PT diagnosis and screening inhibitors or promoters to control excessive  
 PT activation or inhibition for treating e.g. inflammations, autoimmune  
 PT diseases and cancer.  
 XX Claim 4; Page 814-815; 841pp; Japanese.  
 XX The invention relates to a purified protein (I), comprising one of 90  
 CC fully defined sequences (ABP61424-ABP61513) or a protein based on any of  
 CC the sequences but with some amino acids deleted, substituted or added and  
 CC with a NF-kB (nuclear factor kappa B) activating effect. The protein and  
 CC encoding gene (ABQ91912-ABQ92001) are useful in diagnosis and screening  
 CC inhibitors or promoters to control excessive activation or inhibition and

CC for treating e.g. inflammations, autoimmune diseases, cancers,  
CC infections, bone diseases, AIDS, neurodegenerative diseases or ischaemic  
CC disorders

XX Sequence 129 AA;

Query Match 100.0%; Score 203; DB 5; Length 129;  
Best Local Similarity 100.0%; Pred. No. 1.4e-16;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSRSSWSADLDKCMDCASCARPHSDFLGCAA 35  
DB 36 CSRSSWSADLDKCMDCASCARPHSDFLGCAA 70

RESULT 6  
AAU79827  
ID AAU79827 standard; protein; 129 AA.

XX AAU79827;

XX 15-JUL-2002 (first entry)

XX Human type 1 transmembrane protein Fn14.

XX Type 1 transmembrane protein Fn14; human; cytostatic; cardiant;  
KW vulnerary; TWEAK agonist; Fn14 agonist; angiogenesis; tumour progression;  
KW tumour necrosis factor family; TNF family; TWEAK receptor;  
KW myocardial ischaemic condition; myocardial infarction; wound healing;  
KW burn healing; gastric ulcer; tissue transplantation; vascular insufficiency;  
KW organ transplantation; neovascularisation; vascular insufficiency;  
KW cancer; inflammatory macular degeneration; diabetic retinopathy.

OS Homo sapiens.

XX WO20022166-A2.

XX 21-MAR-2002.

XX 12-SEP-2001; 2001WO-US028451.

XX 14-SEP-2000; 2000US-0232355P.

XX (BIOJ ) BIOGEN INC.

XX Browning J, Burkly L, Jakubowski A, Zheng T;

XX WPI; 2002-383103/41.

XX Methods of modulating angiogenesis and inhibiting tumor progression,  
PT using TWEAK receptor agonists.

XX Disclosure; Fig 10A; 37pp; English.

XX The invention describes methods of modulating angiogenesis and inhibiting  
CC tumour progression using TWEAK (a novel member of the tumour necrosis  
CC factor or TNF family) receptor agonists. Conditions which can be treated  
CC using the agonists include myocardial ischaemic conditions (e.g.  
CC myocardial infarction), wound healing (e.g. burn healing and healing of  
CC gastric ulcers), and tissue and organ transplantations to promote  
CC neovascularisation, particularly in subjects suffering from vascular  
CC insufficiency (e.g. diabetic patients). Inhibition of angiogenesis and  
CC subsequently neovascularisation is useful in treatment of cancer,  
CC inflammatory macular degeneration and diabetic retinopathy. This sequence  
CC represents the human type 1 transmembrane protein Fn14, a TWEAK receptor  
CC described in the invention

XX Sequence 129 AA;

Query Match 100.0%; Score 203; DB 5; Length 129;

Best Local Similarity 100.0%; Pred. No. 1.4e-16;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSRSSWSADLDKCMDCASCARPHSDFLGCAA 35  
DB 36 CSRSSWSADLDKCMDCASCARPHSDFLGCAA 70

RESULT 7

ADA56889

ID ADA56889 standard; protein; 129 AA.

XX ADA56889;

XX 20-NOV-2003 (first entry)

XX Human secreted protein #172.

XX immunosuppressive; antiinflammatory; antiasthmatic; antiallergic;  
KW cytostatic; cerebroprotective; neuroprotective; nootropic;  
KW cardiovascular; antiarteriosclerotic; gene therapy;  
KW human secreted protein; immune disorder; inflammation;  
KW respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;  
KW inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;  
KW multiple sclerosis; ischaemic brain injury; Parkinson's disease;  
KW Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;  
KW triple helix formation; antisense gene therapy; forensic biology.

XX Homo sapiens.

XX WO2002102994-A2.

XX 27-DEC-2002.

XX 19-MAR-2002; 2002WO-US008278.

XX 21-MAR-2001; 2001US-0277340P.

XX 19-JUL-2001; 2001US-0306171P.

XX 13-NOV-2001; 2001US-0331287P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM;

XX WPI; 2003-167512/16.

XX N-ESDB; ADA55993.

XX New human secreted polypeptides and polynucleotides, useful for  
PT diagnosing, treating or preventing e.g. immune disorders, inflammatory  
PT conditions, respiratory disorders, cancers, CNS disorders, or  
PT neurodegenerative disorders.

XX Claim 13; SEQ ID NO 1079; 1754pp; English.

XX The invention relates to 592 new human secreted polypeptides useful for  
CC diagnosing, treating or preventing e.g. immune disorders, inflammatory  
CC conditions, respiratory disorders, cancers, CNS disorders, or  
CC neurodegenerative disorders, or polypeptides comprising an amino acid  
CC sequence at least 9% identical to the new sequences. The polypeptides,  
CC antibodies or antibody fragments that bind to the polypeptides, nucleic  
CC acids encoding the polypeptides, agonists or antagonists that binds to  
CC the polypeptide, are useful in preparing diagnostic or pharmaceutical  
CC compositions for diagnosing, treating or preventing an e.g. immune  
CC disorders, inflammatory conditions (e.g. inflammatory bowel disease,  
CC nephritis or Crohn's disease), respiratory disorders (e.g. asthma and  
CC allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders  
CC (e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative  
CC disorders (e.g. Parkinson's disease or Alzheimer's disease), and  
CC cardiovascular disorders (e.g. atherosclerosis or myocarditis). The  
CC polynucleotides are useful for chromosome identification, chromosome  
CC mapping, for controlling gene expression through triple helix formation  
CC or antisense DNA or RNA, in gene therapy, for identifying individuals  
CC from minute biological samples, in forensic biology, and as hybridization  
CC probes. The polypeptides are useful for as molecular weight markers on  
CC sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE)  
CC gels, to raise antibodies, for testing biological activities, and for



CC treating or preventing neural disorders, immune system disorders,  
CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,  
CC renal, proliferative and/or cancerous diseases. This sequence corresponds  
CC to one of the polypeptide of the invention. Note: The sequence data for  
CC this patent did form part of the invention specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 129 AA;

SQ Query Match 100.0%; Score 203; DB 6; Length 129;

Best Local Similarity 100.0%; Pred. No. 1.4e-16;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSRGSSWSADLCKMDCASCRCRPHSDFCLGCAA 35

Db 36 CSRGSSWSADLCKMDCASCRCRPHSDFCLGCAA 70

RESULT 8

ABU56716

ID ABU56716 standard; protein; 129 AA.

XX AC ABU56716;

XX DT 02-APR-2003 (first entry)

XX DE Lung cancer-associated polypeptide #309.

XX KW Lung cancer-associated polypeptide; cytostatic; emphysema;  
XX KW antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;  
XX KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;  
XX KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;  
XX KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.

XX Unidentified.

XX OS WO200286443-A2.

XX PN 31-OCT-2002.

XX PD 18-APR-2002; 2002WO-US012476.

XX PF 18-APR-2001; 2001US-0284770P.

XX PR 10-MAY-2001; 2001US-0290492P.

XX PR 09-NOV-2001; 2001US-0339245P.

XX PR 13-NOV-2001; 2001US-0350666P.

XX PR 29-NOV-2001; 2001US-0334370P.

XX PR 12-APR-2002; 2002US-0372246P.

XX PA (EOSB-) EOS BIOTECHNOLOGY INC.

XX PI Aziz N, Murray R;

XX DR WPI; 2003-093161/08.

XX DR N-PSDB; ABX76445.

XX PT Detecting a lung cancer-associated transcript in a cell from a patient  
XX PT for treating lung cancer, by contacting a biological sample from the  
XX PT patient with a polynucleotide that exhibits increased or decreased  
XX PT expression in lung cancer.

XX PS Claim 27; Page 429; 453pp; English.

XX CC The invention relates to a method for detecting a lung cancer-associated  
XX CC transcript in a cell from a patient, comprising contacting a biological  
XX CC sample from the patient with a polynucleotide that selectively hybridises  
XX CC to a sequence that is at least 80 % identical to a gene that exhibits  
XX CC increased or decreased expression in lung cancer samples. Lung cancer-  
XX CC associated polynucleotides and polypeptides are used for identifying a  
XX CC compound that modulates a lung cancer-associated polypeptide, for  
XX CC inhibiting proliferation of a lung cancer-associated cell to treat lung  
XX CC cancer in a patient and for treating a mammal having lung cancer by

CC administering a modulatory compound identified. The methods are useful  
CC for treating lung cancer, such as small cell lung cancer, non-small cell  
CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,  
CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,  
CC hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and  
CC bronchiectasis. The genes, polynucleotides and polypeptides are useful  
CC for diagnostic purposes and as targets for screening for therapeutic  
CC compounds that modulate lung cancer, such as antibodies. Sequences  
CC ABU56408-ABU56745 represent lung cancer-associated polypeptides of the  
CC invention

XX SQ Sequence 129 AA;

Query Match 100.0%; Score 203; DB 6; Length 129;

Best Local Similarity 100.0%; Pred. No. 1.4e-16;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSRGSSWSADLCKMDCASCRCRPHSDFCLGCAA 35

Db 36 CSRGSSWSADLCKMDCASCRCRPHSDFCLGCAA 70

RESULT 9

ADC74112

ID ADC74112 standard; protein; 129 AA.

XX AC ADC74112;

XX DT 01-JAN-2004 (first entry)

XX DE Human secreted protein - SEQ ID 745.

XX KW antianaemic; antirheumatic; antiarthritic; antiinflammatory; antithyroid;  
XX KW antidiabetic; immunosuppressive; dermatologic; nephrotropic;  
XX KW antiparkinsonian; neuroprotective; nontropic; antibacterial; virucide;  
XX KW fungicide; antiparasitic; antiarteriosclerotic; vulnery; cytostatic;  
XX KW haemopoietic; haematologic; anaemia; autoimmune disorder;  
XX KW rheumatoid arthritis; inflammation; Grave's disease; diabetes;  
XX KW systemic lupus erythematosus; glomerulonephritis; neurodegenerative;  
XX KW Parkinson's; Alzheimer's; wound; hyperproliferative; atherosclerosis;  
XX KW cancer; bacterial; viral; fungal; parasitic infection; gene therapy;  
XX KW human.

XX OS Homo sapiens.

XX PN WO2003038063-A2.

XX PD 08-MAY-2003.

XX PF 19-MAR-2002; 2002WO-US008277.

XX PR 21-MAR-2001; 2001US-0277340P.

XX PR 19-JUL-2001; 2001US-0306171P.

XX PR 13-NOV-2001; 2001US-0331287P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Rosen CA, Ruben SM;

XX DR WPI; 2003-430516/40.

XX DR N-PSDB; ABC73497.

XX PT New human secreted polypeptide for diagnosing, preventing or treating

XX PT hematopoietic or hematologic disorders (e.g. anemia), autoimmune

XX PT disorders (e.g. diabetes) or hyperproliferative disorders (e.g. cancer or

XX PS Claim 16; SEQ ID NO 745; 2272pp; English.

XX CC The invention relates to a novel human secreted polypeptide comprising a

XX CC defined sequence given in the specification. The polypeptide, nucleic

XX CC acid molecule, antibody, agonist or antagonist of the invention may be

XX CC useful for preparing a composition for diagnosing or treating a

CC haemopoietic or haematologic disorder such as anaemia, autoimmune  
CC disorders such as rheumatoid arthritis, inflammation, Grave's disease,  
CC diabetes, systemic lupus erythematosus or glomerulonephritis,  
CC neurodegenerative disorders including Parkinson's disease and Alzheimer's  
CC disease, wounds and hyperproliferative disorders including  
CC atherosclerosis or cancer, as well as bacterial, viral, fungal or  
CC parasitic infections. The polypeptide may also be used during gene  
CC therapy procedures and for identifying a binding partner by contacting  
CC the polypeptide with a binding partner and determining whether the  
CC binding partner increases or decreases the activity of the polypeptide.  
CC The current sequence is that of the human secreted protein of the  
CC invention.

CC SQ Sequence 129 AA;

Query Match 100.0%; Score 203; DB 7; Length 129;

Best Local Similarity 100.0%; Pred. No. 1.4e-16;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSRGSSWSADLDKCMDCASCRCRPHSDFLGCAAA 35

Db 36 CSRGSSWSADLDKCMDCASCRCRPHSDFLGCAAA 70

RESULT 10

ADD37867

ID ADD37867 standard; protein; 129 AA.

XX AC ADD37867;

XX DT 15-JAN-2004 (first entry)

XX DE Human secreted protein #50.

XX KW human secreted protein; Antiallergic; Antiinflammatory; Antibacterial;

XX KW Anti-HIV; Cytostatic; Immunosuppressive; Hemostatic.

XX OS Homo sapiens.

XX PN WO200290526-A2.

XX PD 14-NOV-2002.

XX PF 19-MAR-2002; 2002WO-US008279.

XX PR 21-MAR-2001; 2001US-0277340P.

XX PR 19-JUL-2001; 2001US-0306171P.

XX PR 13-NOV-2001; 2001US-0331287P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Rosen CA, Ruben SM;

XX DR WPI; 2003-140218/13.

XX PT New human secreted proteins and nucleic acid molecules, useful for

XX PT preparing a diagnostic or pharmaceutical composition for diagnosing or

XX PT treating allergic or asthmatic disorders, or related immediate

XX PT hypersensitivity disorders.

XX PS Claim 1; SEQ ID NO 349; 1323pp; English.

XX CC The present invention relates to an isolated polypeptide or human  
XX CC secreted protein. The polypeptides, nucleic acid molecules, antibodies or  
XX CC their fragments, and agonists or antagonists that bind are useful for  
XX CC preparing a diagnostic or pharmaceutical composition for diagnosing or  
XX CC treating allergic or asthmatic disorders. The polypeptide is also useful  
XX CC for identifying a binding partner by contacting the polypeptide with a  
XX CC binding partner, and determining whether the binding partner increases or  
XX CC decreases the activity of the polypeptide. The polypeptides and nucleic  
XX CC acid molecules are also useful for detecting, preventing, diagnosing,  
XX CC prognosticating, treating or ameliorating inflammatory disorders  
XX CC neoplastic diseases, wound healing and disorders of epithelial cell

CC proliferation, immune disorders, cardiovascular disorders, blood-related  
CC disorders, infectious diseases, endocrine disorders, or gastrointestinal  
CC disorders. The nucleic acids are also useful for chromosome  
CC identification, radiation hybrid mapping or long-range restriction  
CC mapping, as molecular weight markers, or as hybridization or diagnostic  
CC probes. The polypeptides and antibodies are useful for providing  
CC immunological probes for differential identification of the tissues  
CC immunohistochemistry assays. The present sequence represents a human  
CC secreted protein.

XX SQ Sequence 129 AA;

Query Match 100.0%; Score 203; DB 7; Length 129;

Best Local Similarity 100.0%; Pred. No. 1.4e-16;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CSRGSSWSADLDKCMDCASCRCRPHSDFLGCAAA 35

Db 36 CSRGSSWSADLDKCMDCASCRCRPHSDFLGCAAA 70

RESULT 11

ADD89033

ID ADD89033 standard; protein; 129 AA.

XX AC ADD89033;

XX DT 29-JAN-2004 (first entry)

XX DE TAT274.

XX KW tumour-associated antigenic target polypeptide; Cytostatic; tumour;

XX KW cancer.

XX OS Homo sapiens.

XX PN WO2003057160-A2.

XX PD 17-JUL-2003.

XX PF 30-DEC-2002; 2002WO-US041798.

XX PR 02-JAN-2002; 2002US-0345444P.

XX PR 25-JAN-2002; 2002US-0351885P.

XX PR 25-FEB-2002; 2002US-0360066P.

XX PR 05-MAR-2002; 2002US-0362004P.

XX PR 20-MAR-2002; 2002US-0366869P.

XX PR 21-MAR-2002; 2002US-0366284P.

XX PR 28-MAR-2002; 2002US-0368679P.

XX PR 19-AUG-2002; 2002US-0404809P.

XX PR 21-AUG-2002; 2002US-0405645P.

XX PA (GETH ) GENENTECH INC.

XX PI Frantz G, Hillan KJ, Phillips H, Polakis P, Smith V, Spencer SD;

XX PI Williams PM, Wu TD, Zhang Z;

XX DR WPI; 2003-569537/53.

XX DR N-PSDB; ADD89109.

XX PT New antibodies against tumor-associated antigenic target polypeptide,

XX PT useful for treating or diagnosing tumors or cancers in mammals, e.g.

XX PT prostate cancer, lung cancer, prostate adenocarcinomas or renal cell

XX PT carcinomas.

XX PS Claim 1; SEQ ID NO 37; 252pp; English.

XX CC The present invention relates to antibodies against tumour-associated  
XX CC antigenic target polypeptide. The antibody is useful for treating or  
XX CC diagnosing tumours or cancers in mammals, e.g. prostate cancer, lung  
XX CC cancer, breast cancer, colon cancer, ovarian cancer, prostate  
XX CC adenocarcinomas, renal cell carcinomas, or pleural mesothelioma. The  
XX CC present sequence represents a TAT polypeptide.

Query Match 100.0%; Score 203; DB 7; Length 129;  
Best Local Similarity 100.0%; Pred. No. 1.4e-16;  
Matches 35; Conservative 0; Mismatches 0; Indels

CC polypeptide of the invention; use of such antibodies for drug targeting;  
CC and methods of screening for modulators of activity or expression of the  
CC polypeptides and nucleic acids. The nucleic acids, polypeptides, and  
CC antibodies and methods are useful for diagnosing, prognosing and treating  
CC cancer and other conditions such as psoriasis, ischaemia, heart disease,  
CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal  
CC neovascularisation syndromes, scarring and uterine fibroids. They may  
CC also be useful in wound healing and in contraception. The present  
CC sequence represents a polypeptide of the invention.

XX Sequence 129 AA;

Query Match 100.0%; Score 203; DB 7; Length 129;

Best Local Similarity 100.0%; Pred. No. 1.4e-16;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSRGSSWSADLDKCMDCASCRCRPHSDFCLGCAA 35

Db 36 CSRGSSWSADLDKCMDCASCRCRPHSDFCLGCAA 70

RESULT 14

ADN39987

ID ADN39987 standard; protein; 129 AA.

XX AC ADN39987;

DT 17-JUN-2004 (first entry)

XX Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C357.

XX Human; differential expression; cancer; angiogenic disorder;  
KW fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;  
KW inflammatory disease; autoimmune disease;  
KW retinal neovascularisation syndrome; scarring; uterine fibroid;  
KW detection; diagnosis; prognosis; drug screening; drug targeting;  
KW wound healing; contraception; cytostatic; cardiant; immunomodulatory;  
KW vulnery; gene therapy; vaccine.

XX Homo sapiens.

OS WO2003042661-A2.

XX 22-MAY-2003.

XX 13-NOV-2002; 2002WO-US036810.

XX 13-NOV-2001; 2001US-0350666P.

XX 21-NOV-2001; 2001US-0332464P.

XX 29-NOV-2001; 2001US-0334393P.

XX 03-DEC-2001; 2001US-0335394P.

XX 14-DEC-2001; 2001US-0340378P.

XX 08-JAN-2002; 2002US-0347211P.

XX 10-JAN-2002; 2002US-0347349P.

XX 08-FEB-2002; 2002US-0355250P.

XX 13-FEB-2002; 2002US-0356714P.

XX 20-FEB-2002; 2002US-0359077P.

XX 29-MAR-2002; 2002US-0368809P.

XX 04-APR-2002; 2002US-0370110P.

XX 12-APR-2002; 2002US-0372246P.

XX 05-JUN-2002; 2002US-0386614P.

XX 16-JUL-2002; 2002US-0396839P.

XX 22-JUL-2002; 2002US-0397775P.

XX 22-JUL-2002; 2002US-0397845P.

XX 09-SEP-2002; 2002US-0409450P.

XX (EOSB-) EOS BIOTECHNOLOGY INC.

XX Afar D. Aziz N. Ginsburg WM. Gish KC. Glynn R. Hevezi PA;

XX Mack DH. Murray R. Watson SR. Wilson KE. Zlotnik A;

XX WPI; 2003-468649/44.

XX N-PSDB; ADN39770.

XX Determining the presence or absence of a pathological cell in a patient,  
PT useful for diagnosing, prognosing or treating cancer, comprises detecting  
PT a nucleic acid in a biological sample.

XX Claim 12; SEQ ID NO C357; 1385pp; English.

XX The invention relates to nucleic acids and proteins (ADN38683-ADN40064)  
CC whose expression is upregulated or downregulated in specific cancers or  
CC other diseases such as angiogenic or fibrotic disorders, and to methods  
CC of determining the presence or absence of a pathological cell in a  
CC patient by detecting a nucleic acid at least 80% identical to those of  
CC the invention or by detecting a polypeptide of the invention. The  
CC invention also relates to expression vectors and host cells comprising a  
CC nucleic acid of the invention; antibodies which specifically bind a  
CC polypeptide of the invention; use of such antibodies for drug targeting;  
CC and methods of screening for modulators of activity or expression of the  
CC polypeptides and nucleic acids. The nucleic acids, polypeptides,  
CC antibodies and methods are useful for diagnosing, prognosing and treating  
CC cancer and other conditions such as psoriasis, ischaemia, heart disease,  
CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal  
CC neovascularisation syndromes, scarring and uterine fibroids. They may  
CC also be useful in wound healing and in contraception. The present  
CC sequence represents a polypeptide of the invention.

XX Sequence 129 AA;

Query Match 100.0%; Score 203; DB 7; Length 129;

Best Local Similarity 100.0%; Pred. No. 1.4e-16;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSRGSSWSADLDKCMDCASCRCRPHSDFCLGCAA 35

Db 36 CSRGSSWSADLDKCMDCASCRCRPHSDFCLGCAA 70

RESULT 15

ABM81706

ID ABM81706 standard; protein; 129 AA.

XX AC ABM81706;

XX 18-NOV-2004 (first entry)

XX Tumour-associated antigenic target (TAT) polypeptide PRO12683, SEQ:4399.

XX Tumour-associated antigenic target; TAT; human; overexpression; cancer;  
KW tumour; diagnosis; cell proliferative disorder; breast cancer;  
KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;  
KW central nervous system cancer; bladder cancer; pancreatic cancer;  
KW cervical cancer; melanoma; leukaemia; hybridisation probe;  
KW chromosome identification; chromosome mapping; gene mapping;  
KW gene therapy; cytostatic.

XX Homo sapiens.

OS WO2004030615-A2.

XX 15-APR-2004.

XX 29-SEP-2003; 2003WO-US028547.

XX 02-OCT-2002; 2002US-0414971P.

XX (GETH) GENENTECH INC.

XX Wu TD, Zhang Z, Zhou Y;

XX WPI; 2004-347921/32.

XX N-PSDB; ACN39936.

XX New tumor-associated antigenic target polypeptides and nucleic acids,  
PT useful in preparing a medicament for treating or detecting a

PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or  
PT prostate cancer or tumor.

XX  
PS Claim 12; SEQ ID NO 4399; 7273pp; English.

XX  
CC The invention relates to human tumour-associated antigenic target (TAT)  
CC polypeptides, and their related nucleic acids. The TAT polypeptides are  
CC overexpressed in cancer tissues compared to normal tissues, and may thus  
CC serve as effective targets for the diagnosis and treatment of cancer in  
CC mammals. The invention also relates to nucleic acid and polypeptide  
CC sequences at least 80% identical to the TAT nucleic acids and  
CC polypeptides; expression vectors and host cells comprising a TAT nucleic  
CC acid; an antibody specific for a TAT polypeptide; a peptide or organic  
CC molecule which binds to a TAT polypeptide; fusion proteins comprising a  
CC TAT polypeptide; and methods and compositions for the treatment or  
CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,  
CC antibodies, antagonists, binding molecules and compositions are useful  
CC for diagnosing or treating a cell proliferative disorder associated with  
CC increased TAT expression, particularly cancers such as breast cancer,  
CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder  
CC cancer, pancreatic cancer, cervical cancer, cancers of the central  
CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be  
CC used as hybridisation probes, in chromosome and gene mapping, in  
CC chromosome identification and in gene therapy. The present sequence  
CC represents a TAT polypeptide of the invention

XX  
SQ Sequence 129 AA;

Query Match 100.0%; Score 203; DB 8; Length 129;  
Best Local Similarity 100.0%; Pred. No. 1.4e-16;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSRGSSWSGADLDKCMDCASCRAHPHSDFCLGCAA 35  
|||  
Db 36 CSRGSSWSGADLDKCMDCASCRAHPHSDFCLGCAA 70

Search completed: February 10, 2005, 18:11:33  
Job time : 56.5702 secs

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OM protein - protein search, using sw model

Run on: February 10, 2005, 18:17:36 ; Search time 40.6798 Seconds  
(without alignments)  
281.128 Million cell updates/sec

Title: US-10-062-831-59\_COPY\_36\_70

Perfect score: 203

Sequence: 1 CSRGSSWSADLCKMDCASCRRPHSDFCLGCAA 35

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1376875 seqs, 326749119 residues

Total number of hits satisfying chosen parameters: 1376875

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
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- 10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep.\*
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- 18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	203	100.0	114	14	US-10-062-831-59
2	203	100.0	114	14	US-10-062-599-59
3	203	100.0	129	9	US-09-742-454A-4
4	203	100.0	129	9	US-09-883-777-4
5	203	100.0	129	14	US-10-024-298A-178
6	203	100.0	129	14	US-10-042-211A-178
7	203	100.0	129	15	US-10-331-496A-37
8	203	100.0	129	15	US-10-295-027-444
9	203	100.0	129	15	US-10-295-027-1305
10	203	100.0	129	15	US-10-617-217A-178
11	203	100.0	300	9	US-09-883-777-9
12	203	100.0	309	9	US-09-742-454A-7
13	203	100.0	309	9	US-09-883-777-7

Sequence 5, Appli  
Sequence 5, Appli  
Sequence 139, App  
Sequence 284, App  
Sequence 228, App  
Sequence 2, Appli  
Sequence 63, Appl  
Sequence 136, App  
Sequence 43, Appl  
Sequence 49, Appl  
Sequence 56, Appl  
Sequence 18, Appl  
Sequence 74, Appl  
Sequence 116, App  
Sequence 2, Appli  
Sequence 17, Appl  
Sequence 16, Appl  
Sequence 2, Appli  
Sequence 76, Appl  
Sequence 7, Appli  
Sequence 125, App  
Sequence 42048, A  
Sequence 2, Appli  
Sequence 2, Appli  
Sequence 538, App  
Sequence 1557, Ap  
Sequence 433, App  
Sequence 433, App  
Sequence 433, App

#### ALIGNMENTS

#### RESULT 1

US-10-062-831-59  
; Sequence 59, Application US/10062831  
; Publication No. US20030105297A1  
; GENERAL INFORMATION:  
; APPLICANT: Steven M. Ruben, et al.  
; TITLE OF INVENTION: 32 Human Secreted Proteins  
; FILE REFERENCE: PZ006P1  
; CURRENT APPLICATION NUMBER: US/10/062,831  
; CURRENT FILING DATE: 2002-02-05  
; PRIOR APPLICATION NUMBER: 09/690,454  
; PRIOR FILING DATE: 1998-11-10  
; PRIOR APPLICATION NUMBER: PCT/US98/10868  
; PRIOR FILING DATE: May 28, 1998  
; PRIOR APPLICATION NUMBER: 60/044,039  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/048,093  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/048,190  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/050,935  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/048,101  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/048,356  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/056,250  
; PRIOR FILING DATE: August 29, 1997  
; PRIOR APPLICATION NUMBER: 60/056,296  
; PRIOR FILING DATE: August 29, 1997  
; PRIOR APPLICATION NUMBER: 60/056,293  
; PRIOR FILING DATE: August 29, 1997  
; NUMBER OF SEQ ID NOS: 229  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 59  
; LENGTH: 114

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; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (114)
; OTHER INFORMATION: Xaa equals stop translation
US-10-062-831-59

Query Match          100.0%; Score 203; DB 14; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.2e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSRGSSWSADLDKCMDCASCARPHSDFCIGCAA 35
   |||||
Db 36 CSRGSSWSADLDKCMDCASCARPHSDFCIGCAA 70

RESULT 2
US-10-062-599-59
; Sequence 59, Application US/10062599
; Publication No. US20030195346A1
; GENERAL INFORMATION:
; APPLICANT: Steven M. Ruben, et al.
; TITLE OF INVENTION: 32 Human Secreted Proteins
; FILE REFERENCE: P2006P1
; CURRENT APPLICATION NUMBER: US/10/062,599
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: 09/690,454
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: 09/189,144
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 60/044,039
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,093
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,190
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/050,935
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,101
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,356
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/056,250
; PRIOR FILING DATE: August 29, 1997
; PRIOR APPLICATION NUMBER: 60/056,296
; PRIOR FILING DATE: August 29, 1997
; PRIOR APPLICATION NUMBER: 60/056,293
; PRIOR FILING DATE: August 29, 1997
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 59
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (114)
; OTHER INFORMATION: Xaa equals stop translation
US-10-062-599-59

Query Match          100.0%; Score 203; DB 14; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.2e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSRGSSWSADLDKCMDCASCARPHSDFCIGCAA 35
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Db 36 CSRGSSWSADLDKCMDCASCARPHSDFCIGCAA 70

RESULT 3
US-09-742-454A-4
; Sequence 4, Application US/09742454A
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; Patent No. US20020041876A1
; GENERAL INFORMATION:
; APPLICANT: WILEY, Steven R.
; TITLE OF INVENTION: TWEAK RECEPTOR
; FILE REFERENCE: 2968-B
; CURRENT APPLICATION NUMBER: US/09/742,454A
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: 60/203,347
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-742-454A-4

Query Match          100.0%; Score 203; DB 9; Length 129;
Best Local Similarity 100.0%; Pred. No. 1.4e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSRGSSWSADLDKCMDCASCARPHSDFCIGCAA 35
   |||||
Db 36 CSRGSSWSADLDKCMDCASCARPHSDFCIGCAA 70

RESULT 4
US-09-883-777-4
; Sequence 4, Application US/09883777
; Patent No. US20020110853A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: TWEAK RECEPTOR
; FILE REFERENCE: 2968-C
; CURRENT APPLICATION NUMBER: US/09/883,777
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: US 60/203,347
; PRIOR FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: PCT/US00/34755
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/742,454
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 129
; TYPE: PRT
; ORGANISM: homo sapiens
; US-09-883-777-4

Query Match          100.0%; Score 203; DB 9; Length 129;
Best Local Similarity 100.0%; Pred. No. 1.4e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSRGSSWSADLDKCMDCASCARPHSDFCIGCAA 35
   |||||
Db 36 CSRGSSWSADLDKCMDCASCARPHSDFCIGCAA 70

RESULT 5
US-10-024-298A-178
; Sequence 178, Application US/10024298A
; Publication No. US20030143540A1
; GENERAL INFORMATION:
; APPLICANT: ASAH KASEI KABUSHIKI KAISHA
; APPLICANT: AKIO MATSUDA
; APPLICANT: GOICHI HONDA
; APPLICANT: SHUJI MURAMATSU
; APPLICANT: YUKIKO NAGANO
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;; TITLE OF INVENTION: NF-K B Activating Gene  
;; FILE REFERENCE: 1254-0191P  
;; CURRENT APPLICATION NUMBER: US/10/024,298A  
;; CURRENT FILING DATE: 2003-04-08  
;; PRIOR APPLICATION NUMBER: 60/314,385  
;; PRIOR FILING DATE: 2001-08-24  
;; PRIOR APPLICATION NUMBER: 60/278,641  
;; PRIOR FILING DATE: 2001-03-26  
;; PRIOR APPLICATION NUMBER: 60/258,315  
;; PRIOR FILING DATE: 2000-12-28  
;; PRIOR APPLICATION NUMBER: JP254018/2001  
;; PRIOR FILING DATE: 2001-08-24  
;; PRIOR APPLICATION NUMBER: JP0088912/2001  
;; PRIOR FILING DATE: 2001-03-26  
;; PRIOR APPLICATION NUMBER: JP402288/2000  
;; PRIOR FILING DATE: 2000-12-28  
;; NUMBER OF SEQ ID NOS: 182  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 178  
;; LENGTH: 129  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-024-298A-178

Query Match 100.0%; Score 203; DB 14; Length 129;  
Best Local Similarity 100.0%; Pred. No. 1.4e-16;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSRGSSWSADLCKMDCASCARPHSDFCIGCAA 35  
DB 36 CSRGSSWSADLCKMDCASCARPHSDFCIGCAA 70

## RESULT 6

US-10-042-211A-178  
;; Sequence 178, Application US/10042211A  
;; Publication No. US20030170719A1  
;; GENERAL INFORMATION:  
;; APPLICANT: MATSUDA, Akio et al.  
;; TITLE OF INVENTION: NFkB Activating Gene  
;; FILE REFERENCE: 1254-0192P  
;; CURRENT APPLICATION NUMBER: US/10/042,211A  
;; CURRENT FILING DATE: 2002-01-11  
;; PRIOR APPLICATION NUMBER: JP 2000-402288  
;; PRIOR FILING DATE: 2000-12-28  
;; PRIOR APPLICATION NUMBER: JP 2001-088912  
;; PRIOR FILING DATE: 2001-03-26  
;; PRIOR APPLICATION NUMBER: JP 2001-254018  
;; PRIOR FILING DATE: 2001-08-24  
;; PRIOR APPLICATION NUMBER: US 60/258,315  
;; PRIOR FILING DATE: 2000-12-28  
;; PRIOR APPLICATION NUMBER: US 60/278,640  
;; PRIOR FILING DATE: 2001-03-26  
;; PRIOR APPLICATION NUMBER: US 60/314,385  
;; PRIOR FILING DATE: 2001-08-24  
;; NUMBER OF SEQ ID NOS: 182  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 178  
;; LENGTH: 129  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-10-042-211A-178

Query Match 100.0%; Score 203; DB 14; Length 129;  
Best Local Similarity 100.0%; Pred. No. 1.4e-16;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSRGSSWSADLCKMDCASCARPHSDFCIGCAA 35  
DB 36 CSRGSSWSADLCKMDCASCARPHSDFCIGCAA 70

## RESULT 7

US-10-331-496A-37  
;; Sequence 37, Application US/10331496A  
;; Publication No. US20030228305A1  
;; GENERAL INFORMATION:  
;; APPLICANT: FRANTZ, GRETCHEN  
;; APPLICANT: HILLAN, KENNETH J.  
;; APPLICANT: PHILLIPS, HEIDI S.  
;; APPLICANT: POLAKIS, PAUL  
;; APPLICANT: SMITH, VICTORIA  
;; APPLICANT: SPENCER, SUSAN D.  
;; APPLICANT: WILLIAMS, P. MICKEY  
;; APPLICANT: WU, THOMAS D.  
;; APPLICANT: ZHANG, ZEMIN  
;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND  
;; FILE REFERENCE: P5014E1-PCT  
;; CURRENT APPLICATION NUMBER: US/10/331,496A  
;; CURRENT FILING DATE: 2002-12-30  
;; PRIOR APPLICATION NUMBER: US 60/345,444  
;; PRIOR FILING DATE: 2002-01-02  
;; PRIOR APPLICATION NUMBER: US 60/351,885  
;; PRIOR FILING DATE: 2002-01-25  
;; PRIOR APPLICATION NUMBER: US 60/360,066  
;; PRIOR FILING DATE: 2002-02-25  
;; PRIOR APPLICATION NUMBER: US 60/362,004  
;; PRIOR FILING DATE: 2002-03-05  
;; PRIOR APPLICATION NUMBER: US 60/366,869  
;; PRIOR FILING DATE: 2002-03-20  
;; PRIOR APPLICATION NUMBER: US 60/366,284  
;; PRIOR FILING DATE: 2002-03-21  
;; PRIOR APPLICATION NUMBER: US 60/368,679  
;; PRIOR FILING DATE: 2002-03-28  
;; PRIOR APPLICATION NUMBER: US 60/404,809  
;; PRIOR FILING DATE: 2002-08-19  
;; PRIOR APPLICATION NUMBER: US 60/405,645  
;; PRIOR FILING DATE: 2002-08-21  
;; NUMBER OF SEQ ID NOS: 95  
;; SEQ ID NO 37  
;; LENGTH: 129  
;; TYPE: PRT  
;; ORGANISM: Homo sapien  
US-10-331-496A-37

Query Match 100.0%; Score 203; DB 15; Length 129;  
Best Local Similarity 100.0%; Pred. No. 1.4e-16;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CSRGSSWSADLCKMDCASCARPHSDFCIGCAA 35  
DB 36 CSRGSSWSADLCKMDCASCARPHSDFCIGCAA 70

## RESULT 8

US-10-295-027-444  
;; Sequence 444, Application US/10295027  
;; Publication No. US20030232350A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Afar, Daniel  
;; APPLICANT: Aziz, Natasha  
;; APPLICANT: Ginsberg, Wendy M.  
;; APPLICANT: Gish, Kurt C.  
;; APPLICANT: Glynn, Richard  
;; APPLICANT: Hevezi, Peter A.  
;; APPLICANT: Mack, David H.  
;; APPLICANT: Murray, Richard  
;; APPLICANT: Watson, Susan R.  
;; APPLICANT: Eos Biotechnology, Inc.  
;; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and  
;; FILE REFERENCE: 018501-012500US  
;; CURRENT APPLICATION NUMBER: US/10/295,027  
;; CURRENT FILING DATE: 2002-11-13  
;; PRIOR APPLICATION NUMBER: US 09/663,733

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; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 444
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-444

Query Match      100.0%; Score 203; DB 15; Length 129;
Best Local Similarity 100.0%; Pred. No. 1.4e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  CSRGSSWSADLDKCMDCASCRCRPHSFCLGCAA 35
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Db      36  CSRGSSWSADLDKCMDCASCRCRPHSFCLGCAA 70

RESULT 9
US-10-295-027-1305
; Sequence 1305, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
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; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1305
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-1305

Query Match      100.0%; Score 203; DB 15; Length 129;
Best Local Similarity 100.0%; Pred. No. 1.4e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  CSRGSSWSADLDKCMDCASCRCRPHSFCLGCAA 35
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Db      36  CSRGSSWSADLDKCMDCASCRCRPHSFCLGCAA 70

RESULT 10
US-10-617-217A-178
; Sequence 178, Application US/10617217A
; Publication No. US20040081986A1
; GENERAL INFORMATION:
; APPLICANT: MATSUDA, Akio et al.
; TITLE OF INVENTION: NF-KB ACTIVATING GENE
; FILE REFERENCE: 1254-0229P
; CURRENT APPLICATION NUMBER: US/10/617,217A
; CURRENT FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: JP 2000-402288
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP 2001-088912
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: JP 2001-254018
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/258,315
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/278,640
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/314,385
; PRIOR FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 178
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-617-217A-178

Query Match      100.0%; Score 203; DB 15; Length 129;
Best Local Similarity 100.0%; Pred. No. 1.4e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  CSRGSSWSADLDKCMDCASCRCRPHSFCLGCAA 35
      |||||||
Db      36  CSRGSSWSADLDKCMDCASCRCRPHSFCLGCAA 70

RESULT 11
US-09-883-777-9
; Sequence 9, Application US/09883777
; Patent No. US20020110853A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: TWEAK RECEPTOR
; FILE REFERENCE: 2968-C
; CURRENT APPLICATION NUMBER: US/09/883,777
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/172,878
; PRIOR FILING DATE: 1999-12-20
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;; PRIOR APPLICATION NUMBER: US 60/203,347  
;; PRIOR FILING DATE: 2000-05-10  
;; PRIOR APPLICATION NUMBER: PCT/US00/34755  
;; PRIOR FILING DATE: 2000-12-19  
;; PRIOR APPLICATION NUMBER: US 09/742,454  
;; PRIOR FILING DATE: 2000-12-19  
;; NUMBER OF SEQ ID NOS: 16  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 9  
;; LENGTH: 300  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Human TWEAK receptor fusion protein construct  
US-09-883-777-9

Query Match 100.0%; Score 203; DB 9; Length 300;  
Best Local Similarity 100.0%; Pred. No. 2.9e-16;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CSRGSSWSADLDKCMDCASCRCRPHSDFCGLGCAA 35  
Db 36 CSRGSSWSADLDKCMDCASCRCRPHSDFCGLGCAA 70

RESULT 12  
US-09-742-454A-7  
;; Sequence 7, Application US/09742454A  
;; Patent No. US20020041876A1  
;; GENERAL INFORMATION:  
;; APPLICANT: WILEY, Steven R.  
;; TITLE OF INVENTION: TWEAK Receptor  
;; FILE REFERENCE: 2968-B  
;; CURRENT APPLICATION NUMBER: US/09/742,454A  
;; CURRENT FILING DATE: 2000-12-19  
;; PRIOR APPLICATION NUMBER: 60/172,878  
;; PRIOR FILING DATE: 1999-12-20  
;; PRIOR APPLICATION NUMBER: 60/203,347  
;; PRIOR FILING DATE: 2000-05-10  
;; NUMBER OF SEQ ID NOS: 7  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 7  
;; LENGTH: 309  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence: human TWEAK  
;; OTHER INFORMATION: receptor fusion protein construct  
US-09-742-454A-7

Query Match 100.0%; Score 203; DB 9; Length 309;  
Best Local Similarity 100.0%; Pred. No. 3e-16;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CSRGSSWSADLDKCMDCASCRCRPHSDFCGLGCAA 35  
Db 36 CSRGSSWSADLDKCMDCASCRCRPHSDFCGLGCAA 70

RESULT 13  
US-09-883-777-7  
;; Sequence 7, Application US/09883777  
;; Patent No. US20020110853A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Wiley, Steven R.  
;; TITLE OF INVENTION: TWEAK RECEPTOR  
;; FILE REFERENCE: 2968-C  
;; CURRENT APPLICATION NUMBER: US/09/883,777  
;; CURRENT FILING DATE: 2001-06-18  
;; PRIOR APPLICATION NUMBER: US 60/172,878  
;; PRIOR FILING DATE: 1999-12-20  
;; PRIOR APPLICATION NUMBER: US 60/203,347  
;; PRIOR FILING DATE: 2000-05-10

;; PRIOR APPLICATION NUMBER: PCT/US00/34755  
;; PRIOR FILING DATE: 2000-12-19  
;; PRIOR APPLICATION NUMBER: US 09/742,454  
;; PRIOR FILING DATE: 2000-12-19  
;; NUMBER OF SEQ ID NOS: 16  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 7  
;; LENGTH: 309  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Human TWEAK receptor fusion protein construct  
US-09-883-777-7

Query Match 100.0%; Score 203; DB 9; Length 309;  
Best Local Similarity 100.0%; Pred. No. 3e-16;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CSRGSSWSADLDKCMDCASCRCRPHSDFCGLGCAA 35  
Db 36 CSRGSSWSADLDKCMDCASCRCRPHSDFCGLGCAA 70

RESULT 14  
US-09-742-454A-5  
;; Sequence 5, Application US/09742454A  
;; Patent No. US20020041876A1  
;; GENERAL INFORMATION:  
;; APPLICANT: WILEY, Steven R.  
;; TITLE OF INVENTION: TWEAK Receptor  
;; FILE REFERENCE: 2968-B  
;; CURRENT APPLICATION NUMBER: US/09/742,454A  
;; CURRENT FILING DATE: 2000-12-19  
;; PRIOR APPLICATION NUMBER: 60/172,878  
;; PRIOR FILING DATE: 1999-12-20  
;; PRIOR APPLICATION NUMBER: 60/203,347  
;; PRIOR FILING DATE: 2000-05-10  
;; NUMBER OF SEQ ID NOS: 7  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 5  
;; LENGTH: 129  
;; TYPE: PRT  
;; ORGANISM: Mus sp.  
US-09-742-454A-5

Query Match 93.6%; Score 190; DB 9; Length 129;  
Best Local Similarity 94.3%; Pred. No. 4.8e-15;  
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 CSRGSSWSADLDKCMDCASCRCRPHSDFCGLGCAA 35  
Db 36 CSRGSSWSADLDKCMDCASCRCRPHSDFCGLGCAA 70

RESULT 15  
US-09-883-777-5  
;; Sequence 5, Application US/09883777  
;; Patent No. US20020110853A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Wiley, Steven R.  
;; TITLE OF INVENTION: TWEAK RECEPTOR  
;; FILE REFERENCE: 2968-C  
;; CURRENT APPLICATION NUMBER: US/09/883,777  
;; CURRENT FILING DATE: 2001-06-18  
;; PRIOR APPLICATION NUMBER: US 60/172,878  
;; PRIOR FILING DATE: 1999-12-20  
;; PRIOR APPLICATION NUMBER: US 60/203,347  
;; PRIOR FILING DATE: 2000-05-10  
;; PRIOR APPLICATION NUMBER: PCT/US00/34755  
;; PRIOR FILING DATE: 2000-12-19  
;; PRIOR APPLICATION NUMBER: US 09/742,454  
;; PRIOR FILING DATE: 2000-12-19  
;; NUMBER OF SEQ ID NOS: 16

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-883-777-5

Query Match      93.6%; Score 190; DB 9; Length 129;
Best Local Similarity 94.3%; Pred. No. 4.8e-15;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CSRGSSWSADLDKCMDCASCAPRPHSDPCLGCAAA 35
        |||||||||||||||||||
Db      36 CSSGSSWSADLDKCMDCASCAPRPHSDPCLGCAAA 70
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Search completed: February 10, 2005, 18:43:37  
Job time : 41.6798 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 10, 2005, 18:02:18 ; Search time 14.4298 Seconds  
(without alignments)  
181.064 Million cell updates/sec

**Title:** US-10-062-831-59 COPY 36 70

Perfect score:

Sequence: 1 CSRGSSWSADLDKCMDCASCRRPHSDFCLGCAA 35

Scoring table: BLOSUM62

scoring cable: BLOSOMB2  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%

Post-processing: Minimum Match 0%  
Maximum Match 100%

Maximum March 1999  
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/iaa/backfiles1.pcp:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	203	100.0	114	4	US-09-690-454-59	Sequence 59, Appl
2	203	100.0	129	4	US-09-883-777-4	Sequence 4, Appl
3	203	100.0	129	4	US-09-949-016-6914	Sequence 6914, Ap
4	203	100.0	129	4	US-09-742-454A-4	Sequence 4, Appl
5	203	100.0	300	4	US-09-883-777-9	Sequence 9, Appl
6	203	100.0	309	4	US-09-883-777-7	Sequence 7, Appl
7	203	100.0	309	4	US-09-742-454A-7	Sequence 7, Appl
8	190	93.6	129	4	US-09-883-777-5	Sequence 5, Appl
9	190	93.6	129	4	US-09-742-454A-5	Sequence 5, Appl
10	104.5	51.5	112	4	US-09-489-847-139	Sequence 139, App
11	104.5	51.5	155	4	US-09-489-847-284	Sequence 284, App
12	104.5	51.5	156	4	US-09-489-847-228	Sequence 228, App
13	68	31.5	248	4	US-09-252-991A-29249	Sequence 29249, A
14	65	32.0	400	4	US-08-252-991A-26145	Sequence 26145, A
15	63.5	31.3	928	1	US-08-442-248-2	Sequence 2, Appl
16	63.5	31.3	928	1	US-08-440-815-2	Sequence 2, Appl
17	63.5	31.3	928	3	US-08-486-449-2	Sequence 2, Appl
18	63.5	31.3	928	4	US-08-578-684-2	Sequence 2, Appl
19	63.5	31.3	1005	2	US-08-469-537A-103	Sequence 103, App
20	59.5	29.3	644	1	US-08-336-708A-9	Sequence 9, Appl
21	59.5	29.3	1210	2	US-08-484-438-7	Sequence 7, Appl
22	59.5	29.3	1210	2	US-08-475-035-4	Sequence 4, Appl
23	59.5	29.3	1210	4	US-09-715-249-2	Sequence 2, Appl
24	58.5	28.8	478	3	US-09-570-454-2	Sequence 2, Appl
25	58.5	28.8	478	4	US-09-867-521-2	Sequence 2, Appl
26	56	27.6	94	3	US-08-851-843A-215	Sequence 215, App
27	56	27.6	94	3	US-08-974-549A-334	Sequence 334, App

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RESULT 2
US-09-883-777-4
; Sequence 4, Application US/09883777
; Patent No. 6727225
; GENERAL INFORMATION:
; APPLICANT: WILEY, Steven R.
; TITLE OF INVENTION: TWEAK RECEPTOR
; FILE REFERENCE: 2968-C
; CURRENT APPLICATION NUMBER: US/09/883,777
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: US 60/203,347
; PRIOR FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: PCT/US00/34755
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/742,454
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 129
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-883-777-4

Query Match      100.0%; Score 203; DB 4; Length 129;
Best Local Similarity 100.0%; Pred. No. 1.2e-17;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CSRGSSWSADLDKCMDCASCRCARPHSDFCIGCAAA 35
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Db      36  CSRGSSWSADLDKCMDCASCRCARPHSDFCIGCAAA 70

RESULT 3
US-09-949-016-6914
; Sequence 6914, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6914
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6914

Query Match      100.0%; Score 203; DB 4; Length 129;
Best Local Similarity 100.0%; Pred. No. 1.2e-17;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CSRGSSWSADLDKCMDCASCRCARPHSDFCIGCAAA 35
      |||||||
Db      36  CSRGSSWSADLDKCMDCASCRCARPHSDFCIGCAAA 70

RESULT 4
US-09-742-454A-4
; Sequence 4, Application US/09742454A
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; Patent No. 6824773
; GENERAL INFORMATION:
; APPLICANT: WILEY, Steven R.
; TITLE OF INVENTION: TWEAK RECEPTOR
; FILE REFERENCE: 2968-B
; CURRENT APPLICATION NUMBER: US/09/742,454A
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: 60/203,347
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-742-454A-4

Query Match      100.0%; Score 203; DB 4; Length 129;
Best Local Similarity 100.0%; Pred. No. 1.2e-17;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CSRGSSWSADLDKCMDCASCRCARPHSDFCIGCAAA 35
      |||||||
Db      36  CSRGSSWSADLDKCMDCASCRCARPHSDFCIGCAAA 70

RESULT 5
US-09-883-777-9
; Sequence 9, Application US/09883777
; Patent No. 6727225
; GENERAL INFORMATION:
; APPLICANT: WILEY, Steven R.
; TITLE OF INVENTION: TWEAK RECEPTOR
; FILE REFERENCE: 2968-C
; CURRENT APPLICATION NUMBER: US/09/883,777
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: US 60/203,347
; PRIOR FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: PCT/US00/34755
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/742,454
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human TWEAK receptor fusion protein construct
US-09-883-777-9

Query Match      100.0%; Score 203; DB 4; Length 300;
Best Local Similarity 100.0%; Pred. No. 2.8e-17;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CSRGSSWSADLDKCMDCASCRCARPHSDFCIGCAAA 35
      |||||||
Db      36  CSRGSSWSADLDKCMDCASCRCARPHSDFCIGCAAA 70

RESULT 6
US-09-883-777-7
; Sequence 7, Application US/09883777
; Patent No. 6727225
; GENERAL INFORMATION:
; APPLICANT: WILEY, Steven R.
; TITLE OF INVENTION: TWEAK RECEPTOR
; FILE REFERENCE: 2968-C
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; CURRENT APPLICATION NUMBER: US/09/883,777  
; CURRENT FILING DATE: 2001-06-18  
; PRIOR APPLICATION NUMBER: US 60/172,878  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: US 60/203,347  
; PRIOR FILING DATE: 2000-05-10  
; PRIOR APPLICATION NUMBER: PCT/US00/34755  
; PRIOR FILING DATE: 2000-12-19  
; PRIOR APPLICATION NUMBER: US 09/742,454  
; PRIOR FILING DATE: 2000-12-19  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7  
; LENGTH: 309  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Human TWEAK receptor fusion protein construct  
US-09-883-777-7

Query Match 100.0%; Score 203; DB 4; Length 309;  
Best Local Similarity 100.0%; Pred. No. 2.9e-17;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CSRGSSWSADLDKCMDCASCRARPHSDFCGLGCAA 35  
Db 36 CSRGSSWSADLDKCMDCASCRARPHSDFCGLGCAA 70

RESULT 7  
US-09-742-454A-7  
; Sequence 7, Application US/09742454A  
; Patent No. 6824773  
; GENERAL INFORMATION:  
; APPLICANT: WILEY, Steven R.  
; TITLE OF INVENTION: TWEAK Receptor  
; FILE REFERENCE: 2968-B  
; CURRENT APPLICATION NUMBER: US/09/742,454A  
; CURRENT FILING DATE: 2000-12-19  
; PRIOR APPLICATION NUMBER: 60/172,878  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: 60/203,347  
; PRIOR FILING DATE: 2000-05-10  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 309  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: human TWEAK  
; OTHER INFORMATION: receptor fusion protein construct  
US-09-742-454A-7

Query Match 100.0%; Score 203; DB 4; Length 309;  
Best Local Similarity 100.0%; Pred. No. 2.9e-17;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 CSRGSSWSADLDKCMDCASCRARPHSDFCGLGCAA 35  
Db 36 CSRGSSWSADLDKCMDCASCRARPHSDFCGLGCAA 70

RESULT 8  
US-09-883-777-5  
; Sequence 5, Application US/09883777  
; Patent No. 6727225  
; GENERAL INFORMATION:  
; APPLICANT: Wiley, Steven R.  
; TITLE OF INVENTION: TWEAK RECEPTOR  
; FILE REFERENCE: 2968-C  
; CURRENT APPLICATION NUMBER: US/09/883,777  
; CURRENT FILING DATE: 2001-06-18

; PRIOR APPLICATION NUMBER: US 60/172,878  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: US 60/203,347  
; PRIOR FILING DATE: 2000-05-10  
; PRIOR APPLICATION NUMBER: PCT/US00/34755  
; PRIOR FILING DATE: 2000-12-19  
; PRIOR APPLICATION NUMBER: US 09/742,454  
; PRIOR FILING DATE: 2000-12-19  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 129  
; TYPE: PRT  
; ORGANISM: Mus sp.  
US-09-883-777-5

Query Match 93.6%; Score 190; DB 4; Length 129;  
Best Local Similarity 94.3%; Pred. No. 4.7e-16;  
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CSRGSSWSADLDKCMDCASCRARPHSDFCGLGCAA 35  
Db 36 CSRGSSWSADLDKCMDCASCRARPHSDFCGLGCAA 70

RESULT 9  
US-09-742-454A-5  
; Sequence 5, Application US/09742454A  
; Patent No. 6824773  
; GENERAL INFORMATION:  
; APPLICANT: WILEY, Steven R.  
; TITLE OF INVENTION: TWEAK Receptor  
; FILE REFERENCE: 2968-B  
; CURRENT APPLICATION NUMBER: US/09/742,454A  
; CURRENT FILING DATE: 2000-12-19  
; PRIOR APPLICATION NUMBER: 60/172,878  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: 60/203,347  
; PRIOR FILING DATE: 2000-05-10  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 129  
; TYPE: PRT  
; ORGANISM: Mus sp.  
US-09-742-454A-5

Query Match 93.6%; Score 190; DB 4; Length 129;  
Best Local Similarity 94.3%; Pred. No. 4.7e-16;  
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CSRGSSWSADLDKCMDCASCRARPHSDFCGLGCAA 35  
Db 36 CSRGSSWSADLDKCMDCASCRARPHSDFCGLGCAA 70

RESULT 10  
US-09-489-847-139  
; Sequence 139, Application US/09489847  
; Patent No. 6476195  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al  
; TITLE OF INVENTION: 98 Human Secreted Proteins  
; FILE REFERENCE: P2031P1  
; CURRENT APPLICATION NUMBER: US/09/489,847  
; CURRENT FILING DATE: 2000-01-24  
; EARLIER APPLICATION NUMBER: PCT/US99/17130  
; EARLIER FILING DATE: 1999-07-29  
; EARLIER APPLICATION NUMBER: 60/094,657  
; EARLIER FILING DATE: 1998-07-30  
; EARLIER APPLICATION NUMBER: 60/095,486  
; EARLIER FILING DATE: 1998-08-05  
; EARLIER APPLICATION NUMBER: 60/096,319

; EARLIER FILING DATE: 1998-08-12  
; EARLIER APPLICATION NUMBER: 60/095,454  
; EARLIER FILING DATE: 1998-08-06  
; EARLIER APPLICATION NUMBER: 60/095,455  
; EARLIER FILING DATE: 1998-08-06  
; NUMBER OF SEQ ID NOS: 376  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 139  
; LENGTH: 112  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-489-847-139

Query Match 51.5%; Score 104.5; DB 4; Length 112;  
Best Local Similarity 90.5%; Pred. No. 1.1e-05;  
Matches 19; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 1 CSRGSSWSADLDKCMDCSC-SC 20  
Db 36 CSRGSSWSADLDKCMDCSTSC 56

RESULT 11  
US-09-489-847-284  
; Sequence 284, Application US/09489847  
; Patent No. 6476195  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al  
; TITLE OF INVENTION: 98 Human Secreted Proteins  
; FILE REFERENCE: PZ031P1  
; CURRENT APPLICATION NUMBER: US/09/489,847  
; EARLIER FILING DATE: 2000-01-24  
; EARLIER APPLICATION NUMBER: PCT/US99/17130  
; EARLIER FILING DATE: 1999-07-29  
; EARLIER APPLICATION NUMBER: 60/094,657  
; EARLIER FILING DATE: 1998-07-30  
; EARLIER APPLICATION NUMBER: 60/095,486  
; EARLIER FILING DATE: 1998-08-05  
; EARLIER APPLICATION NUMBER: 60/096,319  
; EARLIER FILING DATE: 1998-08-12  
; EARLIER APPLICATION NUMBER: 60/095,454  
; EARLIER FILING DATE: 1998-08-06  
; EARLIER APPLICATION NUMBER: 60/095,455  
; EARLIER FILING DATE: 1998-08-06  
; NUMBER OF SEQ ID NOS: 376  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 284  
; LENGTH: 155  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-489-847-284

Query Match 51.5%; Score 104.5; DB 4; Length 155;  
Best Local Similarity 90.5%; Pred. No. 1.5e-05;  
Matches 19; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 1 CSRGSSWSADLDKCMDCSC-SC 20  
Db 36 CSRGSSWSADLDKCMDCSTSC 56

RESULT 12  
US-09-489-847-228  
; Sequence 228, Application US/09489847  
; Patent No. 6476195  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al  
; TITLE OF INVENTION: 98 Human Secreted Proteins  
; FILE REFERENCE: PZ031P1  
; CURRENT APPLICATION NUMBER: US/09/489,847  
; EARLIER FILING DATE: 2000-01-24  
; EARLIER APPLICATION NUMBER: PCT/US99/17130  
; EARLIER FILING DATE: 1999-07-29

; EARLIER APPLICATION NUMBER: 60/094,657  
; EARLIER FILING DATE: 1998-07-30  
; EARLIER APPLICATION NUMBER: 60/095,486  
; EARLIER FILING DATE: 1998-08-05  
; EARLIER APPLICATION NUMBER: 60/096,319  
; EARLIER FILING DATE: 1998-08-12  
; EARLIER APPLICATION NUMBER: 60/095,454  
; EARLIER FILING DATE: 1998-08-06  
; EARLIER APPLICATION NUMBER: 60/095,455  
; EARLIER FILING DATE: 1998-08-06  
; NUMBER OF SEQ ID NOS: 376  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 228  
; LENGTH: 156  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; NAME/KEY: SITE  
; LOCATION: (156)  
; OTHER INFORMATION: Xaa equals stop translation  
US-09-489-847-228

Query Match 51.5%; Score 104.5; DB 4; Length 156;  
Best Local Similarity 90.5%; Pred. No. 1.6e-05;  
Matches 19; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 1 CSRGSSWSADLDKCMDCSC-SC 20  
Db 36 CSRGSSWSADLDKCMDCSTSC 56

RESULT 13  
US-09-252-991A-29249  
; Sequence 29249, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 29249  
; LENGTH: 248  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-29249

Query Match 33.5%; Score 68; DB 4; Length 248;  
Best Local Similarity 39.5%; Pred. No. 0.71;  
Matches 15; Conservative 6; Mismatches 13; Indels 4; Gaps 2;

Qy 1 CSRGSS---WSADLDKCMDCSCRRPHSD-FCIGCAA 34  
Db 80 CWAGAAPTCWSATTCRCGCASSRRRTTGRWCACSA 117

RESULT 14  
US-09-252-991A-26145  
; Sequence 26145, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18



Job time : 15.4298 secs

;; PRIOR APPLICATION NUMBER: US 60/074,788  
;; PRIOR FILING DATE: 1998-02-18  
;; PRIOR APPLICATION NUMBER: US 60/094,190  
;; PRIOR FILING DATE: 1998-07-27  
;; NUMBER OF SEQ ID NOS: 33142  
;; SEQ ID NO 26145  
;; LENGTH: 400  
;; TYPE: PRT  
;; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-26145

Query Match 32.0%; Score 65; DB 4; Length 400;  
Best Local Similarity 44.8%; Pred. No. 2.6;  
Matches 13; Conservative 2; Mismatches 14; Indels 0; Gaps 0;

QY 5 SSWADLDKCMDCASCARPHSDFLGCA 33  
Db 69 SNTATLSPRTSTASCRPMFRCSCACCA 97

RESULT 15  
US-08-442-248-2  
; Sequence 2, Application US/08442248  
; Patent No. 5759863  
; GENERAL INFORMATION:  
; APPLICANT: Caras, Ingrid W.  
; APPLICANT: Winslow, John W.  
; TITLE OF INVENTION: AL-1 Neurotrophic Factor  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080

;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patin (Genentech)  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/442,248  
;; FILING DATE: 15-MAY-1995  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/330128  
;; FILING DATE: 27-OCT-1994  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Torchia, Timothy E.  
;; REGISTRATION NUMBER: 36,700  
;; REFERENCE/DOCKET NUMBER: 920C4  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 415/225-8674  
;; TELEFAX: 415/952-9881  
;; INFORMATION FOR SEQ ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 928 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
US-08-442-248-2

Query Match 31.3%; Score 63.5; DB 1; Length 928;  
Best Local Similarity 31.9%; Pred. No. 9.2;  
Matches 15; Conservative 1; Mismatches 16; Indels 15; Gaps 2;

QY 1 CSRGSSWSADLDKCM-----DCASCR-----ARPHSDFCLGCG 32  
Db 278 CSAEGEWLVPICKCKAGYEKNGTCQVCRPGFFKASPHSQTCSKC 324

Search completed: February 10, 2005, 18:18:46

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Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	70	29.8	346	2	D75303	conserved hypothet
2	68	28.9	683	2	T00872	probable protein k
3	67.5	28.7	587	2	G70893	hypothetical prote
4	61	26.0	519	2	B87353	hypothetical prote
5	61	26.0	992	1	GNVVR3	structural polypro
6	61	26.0	1008	1	GNVUUK	glycoprotein precu
7	60	25.5	262	2	H71390	cytochrome-c oxida
8	60	25.5	516	2	E81789	multidrug resistan
9	60	25.5	529	2	C82487	conserved hypothet
10	60	25.5	730	2	JH0798	fasciclin IV precu
11	59.5	25.3	546	2	T47018	hypothetical prote
12	59.5	25.3	546	2	AG0236	probable membrane
13	59.5	25.3	685	2	S65974	conserved hypothet
14	59	25.1	261	2	T11199	cytochrome-c oxida
15	59	25.1	262	2	S43493	cytochrome-c oxida
16	59	25.1	298	2	AD2768	permease imported
17	59	25.1	311	2	F97548	hypothetical prote
18	58.5	24.9	78	2	E69969	hypothetical prote
19	58.5	24.9	506	2	F83545	hypothetical prote
20	58.5	24.9	543	2	F81665	ADP, ATP carrier p
21	58.5	24.9	587	2	E96702	unknown protein, 6
22	58	24.7	36	2	C45875	M1 class I histoco
23	58	24.7	260	2	F83120	zinc ABC transport
24	58	24.7	388	2	A75318	conserved hypothet
25	58	24.7	445	2	D82184	quinol oxidase, ch
26	58	24.7	520	2	S45702	leukotriene-B4 20-
27	58	24.7	555	2	E70409	carbon starvation
28	58	24.7	597	2	G71373	probable methyl-ac
29	58	24.7	719	2	F96577	hypothetical prote

A:Accession: B87353  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-519 <STO>  
A:Cross-references: UNIPROT:Q9AGX4; GB:AE005673; NID:G13422090; PIDN:AAK2822.1; GSPDB:G

F:514-1008/Product: glycoprotein G2 #status predicted <G2>  
F:977-1008/Domain: transmembrane #status predicted <TM3>  
F:34,70,108,208,493,691,696,912,949/Binding site: carbohydrate (Asn) (covalent) #status

Query Match 26.0%; Score 61; DB 1; Length 1008;  
Best Local Similarity 34.3%; Pred. No. 23;  
Matches 12; Conservative 11; Mismatches 10; Indels 2; Gaps 1;

QY 6 RLLVPLGALSUTFTVLGSLGFLVWRCRRRSS 40  
DB 976 RAIWALGGTVSL--IIGVVIYVFTLCLVKKS 1008

RESULT 7  
H71390  
Cytochrome-c oxidase (BC 1.9.3.1) chain III - common lancelet mitochondrion  
C:Species: mitochondrion Branchiostoma lanceolatum (common lancelet)  
C:Date: 03-Aug-1998 #sequence\_revision 03-Aug-1998 #text\_change 09-Jul-2004  
C:Accession: H71390  
R:Spruyt, N.; Delarbre, C.; Gachelin, G.; Laudet, V.  
Nucleic Acids Res. 26, 3279-3285, 1998  
A:Title: Complete sequence of the amphioxus (Branchiostoma lanceolatum) mitochondrial gene  
A:Reference number: A71390; MUID:98292550; PMID:9628930  
A:Accession: H71390  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-262 <SPR>  
A:CROSS-references: UNIPROT:O47425; GB:Y16474; NID:G3292989; PIDN:CAA76253.1; PID:G32929  
C:Genetics:  
A:Gene: COIII  
A:Genome: mitochondrion  
A:Genetic code: SGC4  
C:Superfamily: cytochrome-c oxidase chain III  
C:Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane  
F:17-35/Domain: transmembrane helix #status predicted <TR01>  
F:42-67/Domain: transmembrane helix #status predicted <TR02>  
F:74-106/Domain: transmembrane helix #status predicted <TR03>  
F:130-153/Domain: transmembrane helix #status predicted <TR04>  
F:157-184/Domain: transmembrane helix #status predicted <TR05>  
F:192-224/Domain: transmembrane helix #status predicted <TR06>  
F:234-257/Domain: transmembrane helix #status predicted <TR07>

Query Match 25.5%; Score 60; DB 2; Length 262;  
Best Local Similarity 35.5%; Pred. No. 9.2;  
Matches 11; Conservative 8; Mismatches 8; Indels 4; Gaps 1;

QY 2 PAPFRL-----WPLGGALSUTFTVLGSLGF 28  
DB 6 PPHWHLVFPSPPLVGGSAFTLTGVLVWF 36

RESULT 8  
E81789  
multidrug resistance translocase NMA2168 [imported] - Neisseria meningitidis (strain Z24  
C:Species: Neisseria meningitidis  
C:Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 09-Jul-2004  
C:Accession: E81789  
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel  
; Holroyd, S.; Jagsels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,  
Nature 404, 502-506, 2000  
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.  
A:Reference number: A81775; MUID:20222556; PMID:10761919  
A:Accession: E81789  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-516 <PAR>  
A:CROSS-references: UNIPROT:Q9JSR9; GB:AL162758; GB:AL157959; NID:G7380672; PIDN:CAB8538  
A:Experimental source: serogroup A, strain Z2491  
C:Genetics:  
A:Gene: emrB; NMA2168  
C:Superfamily: lincomycin-resistance protein lmrB

Query Match 25.5%; Score 60; DB 2; Length 516;

Best Local Similarity 25.7%; Pred. No. 17;  
Matches 18; Conservative 11; Mismatches 15; Indels 26; Gaps 4;

QY 1 PPAPRL--TW-----PILGALS-----LTFVLGSLGFLVWR--RC 34  
DB 139 PPAKRTLALAWMTVVVAVPLGVPILGWIWGNWGWIFFINIPIGIISAWITWKHLKC 198

QY 35 RRERSPPPX 44  
DB 199 RETETVKMPT 208

RESULT 9  
C82487  
conserved hypothetical protein VCA0213 [imported] - Vibrio cholerae (strain N16961 serog  
C:Species: Vibrio cholerae  
C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004  
C:Accession: C82487  
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;  
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F.  
l. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
Nature 406, 477-483, 2000  
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.  
A:Reference number: A82035; MUID:20406833; PMID:10952301  
A:Accession: C82487  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-529 <HEI>  
A:CROSS-references: UNIPROT:Q9KMW5; GB:AE004361; GB:AE003853; NID:G9657600; PIDN:AAF9612  
A:Experimental source: serogroup O1; strain N16961; biotype El Tor  
C:Genetics:  
A:Gene: VCA0213  
A:Map position: 2

Query Match 25.5%; Score 60; DB 2; Length 529;  
Best Local Similarity 40.6%; Pred. No. 17;  
Matches 13; Conservative 5; Mismatches 12; Indels 2; Gaps 1;

QY 11 ILGALSUTFTVLGSLGFLVW--RCRRRSS 40  
DB 86 LGGLSLMTASGATRAFAVWAERKCKDRRSA 117

RESULT 10  
JH0798  
fasciclin IV precursor - American bird grasshopper  
C:Species: Schistocerca americana (American bird grasshopper)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004  
C:Accession: JH0798  
R:Kolodkin, A.; Matthes, D.J.; O'Connor, T.P.; Patel, N.H.; Admon, A.; Bentley, D.; Good  
Neuron 9, 831-845, 1992  
A:Title: Fasciclin IV: Sequence, expression, and function during growth cone guidance in  
A:Reference number: JH0798; MUID:93040225; PMID:1418998  
A:Accession: JH0798  
A:Molecule type: mRNA  
A:Residues: 1-730 <KOL>  
A:CROSS-references: UNIPROT:Q26473; GB:L00709; NID:G160844; PID:G160845  
A:Experimental source: embryo  
C:Comment: This protein plays a role in growth cone guidance in the developing central n  
C:Keywords: glycoprotein; transmembrane protein  
F:1-22/Domain: signal sequence #status predicted <SIG>  
F:23-730/Product: fasciclin IV #status predicted <MAT>  
F:23-627/Domain: extracellular #status predicted <EXT>  
F:628-652/Domain: transmembrane #status predicted <TMM>  
F:653-730/Domain: intracellular #status predicted <INT>  
F:44,71,163,267,360,539/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 25.5%; Score 60; DB 2; Length 730;  
Best Local Similarity 48.4%; Pred. No. 23;  
Matches 15; Conservative 4; Mismatches 8; Indels 4; Gaps 1;

QY 14 GALSUTFTVLGSLGFLVWRCRRRSSPPPX 44  
DB 199 RETETVKMPT 208



Search completed: February 14, 2005, 07:24:03  
Job time : 40 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 14, 2005, 07:14:02 ; Search time 175 seconds  
(without alignments)  
128.751 Million cell updates/sec

Title: US-10-062-831-59\_COPY\_71\_114

Perfect score: 235

Sequence: 1 PPAPFRLWPLIGGALSLE.....LSGFLVWRRCRRRSSPPPX 44

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot\_03:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	199	84.7	129	1 FN14 HUMAN	Q9np84 homo sapien
2	199	84.7	191	2 Q6P2Q4	Q6p2q4 homo sapien
3	168	71.5	129	2 O80XX9	O80xx9 rattus norv
4	164	69.8	129	1 FN14 MOUSE	Q9cr75 m tumor nec
5	76.5	32.6	285	2 Q7ZJG0	Q7zjg0 thermus the
6	71	30.2	473	2 Q98J10	Q98j10 rhizobium l
7	70	29.8	216	2 Q7NRH8	Q7nrh8 chromobacte
8	70	29.8	346	2 Q9RSC0	Q9rsc0 deinococcus
9	70	29.8	631	2 Q7S272	Q7s272 neurospora
10	68	28.9	683	2 O64639	O64639 arabidopsis
11	67.5	28.7	587	2 O53417	O53417 mycobacteri
12	67.5	28.7	587	2 Q7U0Q9	Q7u0q9 mycobacteri
13	67.5	28.7	603	2 Q8VK78	Q8vk78 mycobacteri
14	67	28.5	333	2 Q9BZG3	Q9bzg3 homo sapien
15	67	28.5	372	2 Q65LL2	Q65ll2 bacillus li
16	67	28.5	426	2 Q9BZG2	Q9bzg2 homo sapien
17	66	28.1	433	2 Q82Y76	Q82y76 nitrosomona
18	66	28.1	696	2 Q7XK10	Q7xk10 oryza sativ
19	65	27.7	72	2 Q92MCI	Q92mci rhizobium m
20	65	27.7	515	2 Q7U9M5	Q7u9m5 anopheles g
21	65	27.7	726	2 Q7QC04	Q7qc04 anopheles g
22	64.5	27.4	187	2 Q6L237	Q6l237 picophilius
23	64.5	27.4	260	2 Q8RLL2	Q8rll2 pseudomonas
24	64.5	27.4	756	2 Q64RL1	Q64rl1 bacteroides
25	64.5	27.4	1451	2 Q7R2Y9	Q7r2y9 giardia lam
26	64	27.2	105	2 Q884Q0	Q884q0 pseudomonas
27	64	27.2	264	2 Q9T9H5	Q9t9h5 halocynthia
28	64	27.2	394	2 Q9EQX9	Q9eqx9 rattus norv
29	64	27.2	478	2 Q6K6G5	Q6k6g5 oryza sativ
30	63	26.8	210	2 Q63X19	Q63x19 burkholderi
31	63	26.8	243	2 Q8G9Y8	Q8g9y8 escherichia

#### RESULT 1

ID	FN14_HUMAN	STANDARD;	PRT;	129 AA.
AC	Q9AP84; Q9HCS0;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Tumor necrosis factor receptor superfamily member Fn14 precursor			
DE	(Fibroblast growth factor-inducible immediate-early response protein			
DE	14) (FGF-inducible 14) (Tweak-receptor) (Tweakr).			
GN	Name=TNFRSF12A; Synonyms=FN14;			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Placenta;			
RX	MEDLINE=20216634; PubMed=10751351;			
RA	Feng S.-L.Y., Guo Y., Factor V.M., Thorgerisson S.S., Bell D.W.,			
RA	Testa J.R., Peifley K.A., Winkles J.A.,			
RT	"The Fn14 immediate-early response gene is induced during liver			
RT	regeneration and highly expressed in both human and murine			
RT	hepatocellular carcinomas."			
RL	Am. J. Pathol. 156:1253-1261(2000).			
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).			
RA	Tanaka S., Sugimachi K.;			
RT	"Human homologue of Fn14."			
RL	Submitted (DEC-1999) to the EMBL/GenBank/DBSJ databases.			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Uterus;			
RX	MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Faney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Trimmwood J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalius D.E.,			
RA	Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			

#### ALIGNMENTS

32	63	26.8	262	2	Q8HCU7
33	63	26.8	264	2	Q71LJ1
34	63	26.8	264	2	Q71LR6
35	63	26.8	305	2	Q8ZX90
36	63	26.8	368	1	GF62_HUMAN
37	63	26.8	368	2	Q8TAM0
38	63	26.8	370	1	C244_HUMAN
39	63	26.8	490	2	Q8FE07
40	62.5	26.6	184	2	Q6XN37
41	62.5	26.6	343	2	O88537
42	62.5	26.6	424	2	Q71EB6
43	62.5	26.6	468	2	Q88R15
44	62.5	26.6	610	2	Q943G8
45	62	26.4	168	2	Q96EQ6

Q8hcu7 triops can  
Q71lj1 calcarius m  
Q71lr6 pipilo fusc  
Q8zx90 pyrobaculum  
Q9bzj7 homo sapien  
Q8tamo homo sapien  
Q8fe07 escherichia  
Q6xn37 rhodococcus  
O88537 mus musculu  
Q71eb6 grapevine r  
Q88r15 pseudomonas  
Q943g8 oryza sativ  
Q96eq6 homo sapien

```

RN FUNCTION.
RX MEDLINE=12585797; PubMed=11728344; DOI=10.1016/S1074-7613(01)00232-1;
RA Wiley S.R., Cassiano L., Lofton T., Davis-Smith T., Winkles J.A.,
RA Lindner V., Liu H., Daniel T.O., Smith C.A., Fanslow W.C.;
RT "A novel TNF receptor family member binds TWEAK and is implicated in
RT angiogenesis.";
RL Immunity 15:837-846(2001).
CC -!- FUNCTION: Receptor for TNFSF12/TWEAK. Weak inducer of apoptosis in
CC some cell types. Promotes angiogenesis and the proliferation of
CC endothelial cells. May modulate cellular adhesion to matrix
CC proteins.
CC -!- SUBUNIT: Associates with TRAF1 and TRAF2, and probably also with
CC TRAF3.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q9NP84-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9NP84-2; Sequence=VSP_006519;
CC -!- TISSUE SPECIFICITY: Highly expressed in heart, placenta and
CC kidney. Intermediate expression in lung, skeletal muscle and
CC pancreas.
CC -!- INDUCTION: By FGF-1 and phorbol ester.
CC -!- SIMILARITY: Contains 1 TNFR-Cys repeat.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF191148; AAF69108.1; -;
DR EMBL; AB035480; BAA94792.1; -;
DR EMBL; AB035481; BAB17850.1; -;
DR EMBL; BC002718; AAB02718.1; -;
DR Genew; HGNC:18152; TNFRSF12A.
DR H-InvDB; HIX0012751; -;
DR MIM; 605914; -;
DR GO; GO:0006928; P:cell motility; TAS.
DR GO; GO:0007275; P:development; TAS.
DR InterPro; IPR001368; TNFR_c6.
DR PROSITE; PS00652; TNFR_NGFR_1; FALSE NEG.
DR PROSITE; PS50050; TNFR_NGFR_2; FALSE NEG.
KW Alternative splicing; Angiogenesis; Apoptosis; Cell adhesion;
KW Receptor; Signal; Transmembrane.
FT SIGNAL 1 27 Potential.
FT CHAIN 28 129 Tumor necrosis factor receptor
FT 28 129 superfamily member Fnl4.
FT DOMAIN 28 80 Extracellular (Potential).
FT TRANSMEM 81 101 Potential.
FT DOMAIN 102 129 Cytoplasmic (Potential).
FT REPEAT 36 67 TNFR-Cys (atypical).
FT DISULFID 36 49 Potential.
FT DISULFID 52 67 Potential.
FT VARSPPLIC 33 67 Missing (in isoform 2).
FT FTID=VSP_006519.
SQ SEQUENCE 129 AA; 13911 MW; B3FDFB9C1E1C448 CRC64;
Query Match 84.7%; Score 199; DB 1; Length 129;
Best Local Similarity 84.1%; Pred. No. 5.5e-15;
Matches 37; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
Qy 1 PPAPFLLWPILGGALSITFVLGLSGFLVWRCRRSSPPPX 44
Db 71 PPAPFLLWPILGGALSITFVLGLSGFLVWRCRRREKFTTPI 114
RESULT 2
Q6P2Q4

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ID Q6P2Q4 PRELIMINARY; PRT; 191 AA.
AC Q6P2Q4;
DT 05-JUN-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DB Hypothetical protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haiech F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences".;
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX Strausberg R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC064377; AAB64377.1; -;
KW Hypothetical protein.
FT NON TER 1
FT 1 NON TER 1
SQ SEQUENCE 191 AA; 20092 MW; 75B166C4E5F0FA01 CRC64;
Query Match 84.7%; Score 199; DB 2; Length 191;
Best Local Similarity 84.1%; Pred. No. 7.8e-15;
Matches 37; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
Qy 1 PPAPFLLWPILGGALSITFVLGLSGFLVWRCRRSSPPPX 44
Db 133 PPAPFLLWPILGGALSITFVLGLSGFLVWRCRRREKFTTPI 176
RESULT 3
Q80XX9
ID Q80XX9 PRELIMINARY; PRT; 129 AA.
AC Q80XX9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Type 1 transmembrane protein FNL4 (Hypothetical protein).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC Mueller A.M., Giegerich G.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Pituitary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

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RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Fibrotic gland;  
 RA Strausberg R.;  
 RL Submitted (Oct-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY255102; AAP06753.1; -;  
 DR EMBL; BC060537; AAH60537.1; -;  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR InterPro; IPR002212; Fibrin-assoc.  
 KW Hypothetical protein; Transmembrane.  
 SQ SEQUENCE 129 AA; 13616 NW; 57143F979CD7AC77 CRC64;  
 Query Match 71.5%; Score 168; DB 2; Length 129;  
 Best Local Similarity 70.5%; Pred. No. 1.9e-11;  
 Matches 31; Conservative 3; Mismatches 10; Indels 0; Gaps 0;  
 QY 1 PPAPFLPPIGGALSLFTVLGLSLGFLVWRCRRERSPPPX 44  
 DB 71 PPAPFLPPIGGALSLVLLVSLVGLVWRCRRERKFTTPI 114  
 RESULT 4  
 ID FN14 MOUSE STANDARD; PRT; 129 AA.  
 AC Q9C975; O9Q2W3;  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member Fn14 precursor  
 DE (Fibroblast growth factor-inducible immediate-early response protein 2)  
 DE 14) (FGF-inducible 14) (Fibroblast growth factor regulated protein 2)  
 DE (Tweak-receptor) (TweakR).  
 GN Name=Fn14; Synonyms=Fgfr2, Fn14;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Craniognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Balb/c; TISSUE=Fibroblast;  
 RX MEDLINE=20020297; PubMed=10551889; DOI=10.1074/jbc.274.46.33166;  
 RA Meighan-Mantha R.L., Hsu D.K.W., Guo Y., Brown S.A.N., Feng S.-L.Y.,  
 RA Peilely K.A., Alberts G.F., Copeland N.G., Gilbert D.J., Jenkins N.A.,  
 RA Richards C.M., Winkles J.A.;  
 RA "The mitogen-inducible Fn14 gene encodes a type I transmembrane  
 RT protein that modulates fibroblast adhesion and migration.";  
 RL J. Biol. Chem. 274:33166-33176(1999).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Placenta;  
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
 RA Okazaki Y., Furuno N., Kasukawa T., Adachi J., Bono H., Kondo S.,  
 RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
 RA Schirali L.M., Kanapin A., Mutsaers H., Batalov S., Beisel K.W.,  
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,  
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
 RA Gramond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
 RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,  
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,  
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shinada K.,  
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
 RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
 RA Birney E., Hayashizaki Y.;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs.";  
 RL Nature 420:563-573(2002).  
 [3]  
 RN SEQUENCE FROM N.A.  
 RP TISSUE=Breast tumor;  
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 [3]  
 CC -!- FUNCTION: Receptor for TNFSF12/TWEAK (By similarity). Weak inducer  
 CC of apoptosis in some cell types. Promotes angiogenesis and the  
 CC proliferation of endothelial cells. May modulate cellular adhesion  
 CC to matrix proteins.  
 CC -!- SUBUNIT: Associates with TRAF1 and TRAF2, and probably also with  
 CC TRAF3 (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- TISSUE SPECIFICITY: Highly expressed in fetal heart, intestine,  
 CC kidney, liver, lung and skin, and in adult heart and ovary.  
 CC Intermediate expression in adult kidney, lung and skin.  
 CC -!- INDUCTION: By FGF-1.  
 CC -!- SIMILARITY: Contains 1 TNFR-Cys repeat.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See http://www.isb-sib.ch/announce/  
 CC or send an email to license@isb-sib.ch).  
 CC -----  
 CC EMBL; AF156164; AAF07882.1; -;

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DR EMBL; AK005530; BAB24101.1; -.
DR EMBL; AK005382; BAB23989.1; -.
DR EMBL; BC025860; AAH25860.1; -.
DR MGD; MGI:1351484; Tfrs1f12a.
DR GO; GO:0001726; C:ruffles; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0007155; P:cell adhesion; IDA.
DR GO; GO:0045773; P:positive regulation of axon extension; IDA.
DR GO; GO:0006931; P:substrate-bound cell migration, cell attach. .; IDA.
DR InterPro; IPR001368; TNFR_C6.
DR PROSITE; PS00652; TNFR_NGFR_1; FALSE NEG.
DR PROSITE; PS00500; TNFR_NGFR_2; FALSE NEG.
KW Angiogenesis; Apoptosis; Cell adhesion; Receptor; Signal;
KW Transmembrane.
FT SIGNAL 1 27 Potential.
FT CHAIN 28 129 Tumor necrosis factor receptor
FT 28 129 superfamily member Fn14.
FT DOMAIN 28 80 Extracellular (Potential).
FT TRANSMEM 81 101 Potential.
FT DOMAIN 102 129 Cytoplasmic (Potential).
FT REPEAT 36 67 TNFR-Cys (atypical).
FT DISULFID 36 49 Potential.
FT DISULFID 52 67 Potential.
FT CONFLICT 3 4 SA -> PG (in Ref. 1).
SQ SEQUENCE 129 AA; 13641 MW; 1665C68B4D9A9253 CRC64;

Query Match 69.8%; Score 164; DB 1; Length 129;
Best Local Similarity 70.5%; Pred. No. 5.4e-11;
Matches 31; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

QY 1 PPAPRLWPILGGALSTFVLGLSGFLVWRRCRRSSPPX 44
DB 71 PPAHRLWPILGGALSLVLVALVSSFLVWRRCRRKFTTPI 114

RESULT 5
Q72JG0 PRELIMINARY; PRT; 285 AA.
AC Q72JG0
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
GN OrderedLocusNames=TT00812;
OS Thermus thermophilus (strain HB27 / ATCC BAA-163 / DSM 7039).
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OC Thermus.
OX NCBI_TaxID=262724;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15064768;
RA Henne A., Brueggemann H., Raasch C., Wieser A., Hartesch T.,
RA Liesegang H., Johann A., Lienard T., Gohl O., Martinez-Arias R.,
RA Jacobi C., Starkuviene V., Schlenczek S., Dencker S., Huber R.,
RA Klenk H.-P., Kramer W., Merkl R., Gottschalk G., Fritz H.-J.;
RT "The genome sequence of the extreme thermophile Thermus
RT thermophilus.";
RL Nat. Biotechnol. 22:547-553(2004).
DR EMBL; AE017303; AAS81158.1; -.
DR InterPro; IPR010982; Lambda_like_DNA.
KW Complete proteome.
SQ SEQUENCE 285 AA; 31440 MW; C3C8A7292A7D6C24 CRC64;

Query Match 32.6%; Score 76.5; DB 2; Length 285;
Best Local Similarity 43.8%; Pred. No. 0.99;
Matches 21; Conservative 5; Mismatches 15; Indels 7; Gaps 3;

QY 1 PPAPRLWPILGGALSTFVLGLL-SGFLVWRRCR---RSPSPX 44
DB 83 PPRPRRLWPMU---LALLGLFLYAGFLWPRPKVKVLPDP 127

RESULT 6

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Q98JTO
ID Q98JTO PRELIMINARY; PRT; 473 AA.
AC Q98JTO
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE M111933 protein.
GN OrderedLocusNames=m111933;
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsuoto M., Matsuoto M.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti.";
RL DNA Res. 7:331-338(2000).
DR EMBL; AP002998; BAB49185.1; -.
DR InterPro; IPR002810; DUF107.
DR Pfam; PF01957; MfeD; 1.
KW Complete proteome.
SQ SEQUENCE 473 AA; 48746 MW; 2C466F3B41A49AF5 CRC64;

Query Match 30.2%; Score 71; DB 2; Length 473;
Best Local Similarity 39.5%; Pred. No. 6.5;
Matches 15; Conservative 6; Mismatches 13; Indels 4; Gaps 1;

QY 5 FRLWLPILGGALSTFVLGLSGFLVWRRCRRSSPP 42
DB 371 FAMSVAIVGPAALTGLALLTGYVW---AARKNPP 404

RESULT 7
Q7NRH8 PRELIMINARY; PRT; 216 AA.
AC Q7NRH8
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=CV3803;
OS Chromobacterium violaceum.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Chromobacterium.
OX NCBI_TaxID=536;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 12472 / DSM 30191;
RX MEDLINE=22882880; PubMed=14500782; DOI=10.1073/pnas.1832124100;
RA Vasconcelos A.T.R., de Almeida D.F., Hungria M., Guimaraes C.T.,
RA Antonio R.V., Almeida F.C., de Almeida L.G.P., de Almeida R.,
RA Alves-Gomes J.A., Andrade E.M., Araripe J., de Araujo M.F.F.,
RA Astolfi-Filho S., Azevedo V., Baptista A.J., Bataus L.A.M.,
RA Batista J.S., Belo A., van den Berg C., Bogo M., Bonatto S.,
RA Bordignon J., Brígido M.M., Brito C.A., Brocchi M., Burity H.A.,
RA Canargo A.A., Cardoso D.D.P., Carneiro N.P., Carraro D.M.,
RA Carvalho C.M.B., Cascado J.C.M., Cavada B.S., Chueire L.M.O.,
RA Creczynski-Pasa T.B., Cunha-Junior N.C., Fagundes N., Falcao C.L.,
RA Fantinatti F., Farias I.P., Felipe M.S., Ferrari L.P., Ferro J.A.,
RA Ferro M.I.T., Franco G.R., Freitas N.S.A., Furlan L.R.,
RA Garzinelli R.T., Gomes E.A., Goncalves P.R., Grangeiro T.B.,
RA Grattapaglia D., Grisard E.C., Hanna E.S., Jardim S.N., Laurino J.,
RA Ieoi L.C.M.F., Lima L.F.A., Loureiro M.F., Lyra M.C.C.P.,
RA Madeira H.M.F., Manfio G.P., Maranhao A.Q., Martins W.S.,
RA di Mauro S.M.Z., de Medeiros S.R.B., Meissner R.V., Moreira M.A.M.,
RA Nascimento F.F., Nicolas M.F., Oliveira J.G., Oliveira S.C.,

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RA Paixao R.F.C., Parente J.A., Pedrosa F.O., Pena S.D.J., Pereira J.O.,  
 RA Pereira M., Pinto L.S.R.C., Pinto L.S., Porto J.I.R., Potrich D.P.,  
 RA Ramalho-Neto C.E., Reis A.M.M., Rigo L.U., Rondinelli E.,  
 RA Santos E.B.P., Santos F.R., Schneider M.P.C., Seunanez H.N.,  
 RA Silva A.M.R., da Silva A.L.C., Silva D.W., Silva R., Simoes I.C.,  
 RA Simon D., Soares C.M.A., Soares R.B.A., Souza E.M., Souza K.R.L.,  
 RA Souza R.C., Steffens M.B.R., Steindel M., Teixeira S.R., Urmenyi T.,  
 RA Vettore A., Wassen R., Zaha A., Simpson A.J.G.;  
 RT "The complete genome sequence of *Chromobacterium violaceum* reveals  
 RT remarkable and exploitable bacterial adaptability";  
 RL Proc. Natl. Acad. Sci. U.S.A. 100:11660-11665(2003).  
 DR EMBL; A016923; AAQ61465.1; -;  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0005293; F:lysine permease activity; IEA.  
 DR GO; GO:0006865; P:amino acid transport; IEA.  
 DR InterPro; IPR001123; LySE.  
 DR Pfam; PF01810; LySE; 1.  
 KW Complete proteome; Hypothetical protein.  
 SQ SEQUENCE 216 AA; 22482 MW; 73BF6D92977F7825 CRC64;  
 Query Match 29.8%; Score 70; DB 2; Length 216;  
 Best Local Similarity 47.5%; Pred. No. 4.3;  
 Matches 19; Conservative 3; Mismatches 18; Indels 0; Gaps 0;  
 QY 2 PAPFLLPILGGALSLTFLVGLSGFLVWRRCRRERSPP 41  
 Db 70 PALFAVKYIGGYLAWLGVNMLKSGILAWRRARRGDESP 109  
 RESULT 8  
 ID Q9RSC0 PRELIMINARY; PRT; 346 AA.  
 AC Q9RSC0;  
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
 DE Hypothetical protein DR2205.  
 GN OrderedLocustNames=DR2205;  
 OS Deinococcus radiodurans.  
 OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;  
 OC Deinococcaceae; Deinococcus.  
 OX NCBI\_TaxID=1299;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=R1 / ATCC 13939 / DSM 20539 / NCIB 9279;  
 RX MEDLINE=20036896; PubMed=10567266; DOI=10.1126/science.286.5444.1571;  
 RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,  
 RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,  
 RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,  
 RA Vamathevan J.J., Lam P., McDonald L.A., Utterback T.R., Zaleski C.,  
 RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,  
 RA Ketchum K.A., Nelson K.E., Salzberg S.L., Smith H.O., Venter J.C.,  
 RA Fraser C.M.;  
 RT "Genome sequence of the radioresistant bacterium *Deinococcus*  
 RT radiodurans R1";  
 RL Science 286:1571-1577(1999).  
 DR EMBL; AE002053; AAF11754.1; -;  
 DR PIR; D75303; D75303.  
 DR TIGR; DR2205; -;  
 KW Complete proteome; Hypothetical protein.  
 SQ SEQUENCE 346 AA; 36056 MW; 1F6C08A36C46F01F CRC64;  
 Query Match 29.8%; Score 70; DB 2; Length 346;  
 Best Local Similarity 37.2%; Pred. No. 6.4;  
 Matches 16; Conservative 7; Mismatches 20; Indels 0; Gaps 0;  
 QY 2 PAPFLLPILGGALSLTFLVGLSGFLVWRRCRRERSPPPP 44  
 Db 148 PAPFLALAVSGGAALSVLALGALGAWHSTRARPHLAAPPH 190  
 RESULT 9  
 Q7S272

ID Q7S272 PRELIMINARY; PRT; 631 AA.  
 AC Q7S272;  
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
 DE Hypothetical protein.  
 GN Name=NCU09651.1;  
 OS Neurospora crassa.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.  
 OX NCBI\_TaxID=5141;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=OR74A;  
 RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,  
 RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehm B.,  
 RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,  
 RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,  
 RA Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,  
 RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,  
 RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,  
 RA Kanal M., Kamysasellis M., Mauceli E., Bielke C., Rudd S., Frisman D.,  
 RA Krystofova S., Rasmussen C., Metsenbergh R.L., Perkins D.D., Kroken S.,  
 RA Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A.,  
 RA DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,  
 RA Varden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,  
 RA Natvig D.O., Alex L.A., Mannhaupt G., Eboole D.J., Freitag M.,  
 RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.,  
 RT "The Genome Sequence of the Filamentous Fungus *Neurospora crassa*."  
 RL Nature 0:0-0(2003).  
 CC -!- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 DR EMBL; AABX01000430; EAA29481.1; -;  
 DR InterPro; IPR011043; Gal\_oxid\_central.  
 KW Hypothetical protein.  
 SQ SEQUENCE 631 AA; 68228 MW; B7CE72E9DF6A7677 CRC64;  
 Query Match 29.8%; Score 70; DB 2; Length 631;  
 Best Local Similarity 30.2%; Pred. No. 11;  
 Matches 16; Conservative 10; Mismatches 9; Indels 18; Gaps 2;  
 QY 10 PILGGAL-SLTFLVGLSGFLVWRRCRRERS-----SPPPX 44  
 Db 521 PIVGGVGVVGLVGVIGVGLFWRRNKKNSAGALSSAELPVQBPSPPPQ 573  
 RESULT 10  
 ID O64639 PRELIMINARY; PRT; 683 AA.  
 AC O64639;  
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)  
 DE Hypothetical protein At2g45590.  
 GN Name=At2g45590;  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Lin X., Kaul S., Town C.D., Benito M.-I., Creasy T.H., Haas B.-J.,  
 RA Wu D., Maiti R., Ronning C.M., Koo H., Fujii C.Y., Utterback T.R.,  
 RA Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Town C.D., Kaul S.;  
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.

[illegible]

RT	"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";		
RL	Nature 393:537-544 (1998).		
DR	EMBL; BX842575; CAA17185.1; --		
DR	PIR; C70893; C70893.		
DR	Tuberculist; Rv1069c; --		
KW	Complete proteome.		
SW	SEQUENCE 587 AA; 64341 MW; DB13451EF3C3EEC6 CRC64;		
Query Match	28.7%; Score 67.5; DB 2; Length 587;		
Best Local Similarity	31.6%; Pred. No. 20;		
Matches	24; Conservative 3; Mismatches 16; Indels 33; Gaps 4;		
QY	2 PAPFLLWPI-----LGGALSITFV-----LGLLSG-----FLV 30		
DB	35 PQPIRSTWTWIRHYTFTGTAMGLVFVWFSMTPSLLPRGFLPQGLVSGICGAFGYGLGVFAV 94		
QY	31 W--RRCRERSPPPP 44		
DB	95 WLVRVYMRSHNSPPPP 110		
RESULT 12			
Q7U0Q9	PRELIMINARY; PRT; 587 AA.		
ID	Q7U0Q9;		
AC	Q7U0Q9;		
DT	01-OCT-2003 (TrEMBLrel. 25, Created)		
DT	01-OCT-2003 (TrEMBLrel. 25, Last sequence update)		
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)		
DE	Hypothetical protein Mb1098c.		
GN	OrderedLocusNames=Mb1098c;		
OS	Mycobacterium bovis.		
OC	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;		
OC	Corynebacterineae; Mycobacteriaceae; Mycobacterium.		
OX	NCBI_TaxID=1765;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=AF2122/97;		
RX	MEDLINE=22709107; PubMed=12788972; DOI=10.1073/pnas.1130426100;		
RA	Garnier T., Bigmeier K., Camus J.-C., Medina N., Mansoor H.,		
RA	Pryor M., Duthoy S., Gronin S., Lacroix C., Monsemp C., Simon S.,		
RA	Harris B., Ackin R., Boggett J., Mayes R., Keating L., Wheeler P.R.,		
RA	Parkhill J., Barrrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;		
RT	"The complete genome sequence of Mycobacterium bovis."		
RL	Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).		
DR	EMBL; BX248337; CAD93958.1; --		
KW	Complete proteome; Hypothetical protein.		
SW	SEQUENCE 587 AA; 64341 MW; DB13451EF3C3EEC6 CRC64;		
Query Match	28.7%; Score 67.5; DB 2; Length 587;		
Best Local Similarity	31.6%; Pred. No. 20;		
Matches	24; Conservative 3; Mismatches 16; Indels 33; Gaps 4;		
QY	2 PAPFLLWPI-----LGGALSITFV-----LGLLSG-----FLV 30		
DB	35 PQPIRSTWTWIRHYTFTGTAMGLVFVWFSMTPSLLPRGFLPQGLVSGICGAFGYGLGVFAV 94		
QY	31 W--RRCRERSPPPP 44		
DB	95 WLVRVYMRSHNSPPPP 110		
RESULT 13			
Q8VK78	PRELIMINARY; PRT; 603 AA.		
ID	Q8VK78;		
AC	Q8VK78;		
DT	01-MAR-2002 (TrEMBLrel. 20, Created)		
DT	01-MAR-2002 (TrEMBLrel. 20, Last sequence update)		
DT	01-MAR-2002 (TrEMBLrel. 20, Last annotation update)		
DE	Hypothetical protein.		
GN	OrderedLocusNames=Mt1099;		
OC	Mycobacterium tuberculosis.		
OC	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;		

OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.

RN NCBI\_TaxID=1773;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CDC 1551 / Oehkosh;  
 RX MEDLINE=22206494; PubMed=12218036;  
 RX DOI=10.1128/JB.184.19.5479-5490.2002;  
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,  
 RA Peterson J.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D.H.,  
 RA Hickey E.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D.,  
 RA Salzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Khouri H.M.,  
 RA Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C.,  
 RA Fraser C.M.;  
 RT "Whole-genome comparison of Mycobacterium tuberculosis clinical and  
 RT laboratory strains.";  
 RL J. Bacteriol. 184:5479-5490(2002).  
 DR EMBL; AE000516; AAK45355.1; --  
 DR TIGR; MT1099; --  
 KW Hypothetical protein.  
 SQ SEQUENCE 603 AA; 66149 MW; F3C1A57609BEAB69 CRC64;

Query Match 28.7%; Score 67.5; DB 2; Length 603;  
 Best Local Similarity 31.6%; Pred. No. 20;  
 Matches 24; Conservative 3; Mismatches 16; Indels 33; Gaps 4;  
 QY 2 PAPFRLWPI-----LGGALSLTFV-----LGLLSG-----FLV 30  
 DB 35 PPTIRSTWIRHYTGTAMGLVFWFMSPTSLPRGLFQGLVSGICGARGYGIVFAV 94  
 QY 31 W--RCRRERSPPPX 44  
 DB 95 WLVRMRSHNSPPPX 110

RESULT 14

Q9BZG3 PRELIMINARY; PRT; 333 AA.  
 AC Q9BZG3;  
 DT 01-JUN-2001 (TReMBLrel. 17, Created)  
 DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)  
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)  
 DE Acid phosphatase variant 3.  
 GN Name=ACPT;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21309073; PubMed=11414767; DOI=10.1006/geno.2001.6556;  
 RX Yousef G.M., Diamandis M., Jung K., Diamandis E.P.;  
 RT "Molecular cloning of a novel human acid phosphatase gene (ACPT) that  
 RT is highly expressed in the testis.";  
 RL Genomics 74:385-395(2001).  
 DR EMBL; AF321918; AAK09396.1; --  
 DR HSSP; P15309; IND6.  
 DR GO; GO:0003993; F:acid phosphatase activity; IEA.  
 DR InterPro; IPR000560; HisAc.phosphatase.  
 DR Pfam; PF00328; Acid phosphatase; 1.  
 DR PROSITE; PS00616; HIS\_ACID\_PHOSPHAT\_1; 1.  
 DR PROSITE; PS00778; HIS\_ACID\_PHOSPHAT\_2; UNKNOWN 1.  
 SQ SEQUENCE 333 AA; 35402 MW; 0C0237096567B30F CRC64;

Query Match 28.5%; Score 67; DB 2; Length 333;  
 Best Local Similarity 40.5%; Pred. No. 14;  
 Matches 17; Conservative 5; Mismatches 16; Indels 4; Gaps 2;  
 QY 1 PPAPFRLWPIGGALSLTFVLGLLSGFLVWR--RCRRERSPP 41  
 DB 294 PPAP---VVPILAGAVAVIALSLGLGLAWRPGCLRALGSP 332

RESULT 15

Q65LL2 PRELIMINARY; PRT; 372 AA.  
 AC Q65LL2;  
 DT 25-OCT-2004 (TReMBLrel. 28, Created)  
 DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)  
 DE 25-OCT-2004 (TReMBLrel. 28, Last annotation update)  
 DE YhjN (Proteinase inhibitor I4, serpin).  
 GN Name=YhjN; ORFNames=BL01326, BLI01144;  
 OS Bacillus licheniformis DSM 13.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=279010;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=DSM 13;  
 RX PubMed=15383718;  
 RA Veith B., Herzberg C., Steckel S., Feesche J., Maurer K.H.,  
 RA Ehrenreich P., Baumeister S., Henne A., Liesegang H., Merkl R.,  
 RA Ehrenreich A., Gottschalk G.;  
 RT "The Complete Genome Sequence of Bacillus licheniformis DSM13, an  
 RT Organism with Great Industrial Potential.";  
 RL J. Mol. Microbiol. Biotechnol. 7:204-211(2004).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 14580;  
 RA Rey M.W., Ramaiya P., Nelson B.A., Brody-Karpin S.D., Zaretsky E.J.,  
 RA Tang M., de Leon A.L., Xiang H., Gusti V., Clausen I.G., Olsen P.B.,  
 RA Rasmussen M.D., Andersen J.T., Jorgensen P.L., Larsen T.S.,  
 RA Sorokin A., Bolotin A., Lapidus A., Galleron N., Ehrlich S.D.,  
 RA Berka R.M.;  
 RT "Complete genome sequence of the industrial bacterium Bacillus  
 RT licheniformis and comparisons with closely related Bacillus species.";  
 RL Genome Biol. 5:R77-R77(2004).  
 DR EMBL; AE017333; AAU40052.1; --  
 DR EMBL; CP000002; AAU22705.1; --  
 SQ SEQUENCE 372 AA; 39272 MW; AD3D10B8EBB6CFAB CRC64;  
 Query Match 28.5%; Score 67; DB 2; Length 372;  
 Best Local Similarity 46.4%; Pred. No. 15;  
 Matches 13; Conservative 6; Mismatches 9; Indels 0; Gaps 0;  
 QY 5 PRLWPIGGALSLTFVLGLLSGFLVWR 32  
 DB 77 FKENWLVGVMLLSVVFAMLSGFLVWR 104  
 Search completed: February 14, 2005, 07:23:19  
 Job time : 177 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 14, 2005, 07:13:22 ; Search time 164 Seconds  
(without alignments)  
103.765 Million cell updates/sec

Title: US-10-062-831-59\_COPY\_71\_114

Perfect score: 235  
Sequence: 1 PPAPRLWPLILGALSITF.....LSGFLVWRCRRSSPPPX 44

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	235	100.0	114	2	AAW73409 Human sec
2	199	84.7	94	7	ABU64233 Human CRY
3	199	84.7	129	2	AAW88506 Human liv
4	199	84.7	129	3	AAV57940 Human tra
5	199	84.7	129	4	AAU03498 Human TWE
6	199	84.7	129	5	ABP61512 Human NF-
7	199	84.7	129	6	AAU79827 Human typ
8	199	84.7	129	5	ADA56889 Human sec
9	199	84.7	129	6	ABU56716 Lung canc
10	199	84.7	129	7	ADC74112 Human sec
11	199	84.7	129	7	ADD37867 Human sec
12	199	84.7	129	7	ADD89033 TAT274.1
13	199	84.7	129	7	ABU64232 Human FRA
14	199	84.7	129	7	ADN39126 Cancer/an
15	199	84.7	129	7	ADN39987 Cancer/an
16	199	84.7	129	8	ABM81706 Tumour-as
17	164	69.8	129	5	AAU79828 Mouse typ
18	68	28.9	683	3	AGC30077 Arabidops
19	68	28.9	683	5	ABB92130 Herbicida
20	67	28.5	333	5	ABG32546 Human tes
21	67	28.5	375	5	ABG32542 Human tes
22	67	28.5	426	4	ABG23348 Novel hum
23	67	28.5	426	5	AAU75788 Human pro
24	67	28.5	426	5	ABG32541 Human tes
25	67	28.5	426	5	AAU09880 Novel hum

26	67	28.5	426	8	ADS10721	Human the
27	64.5	27.4	351	8	ADH58984	Rat GPCR
28	64.5	27.4	351	8	ADI53331	Rat FPR1
29	64.5	27.4	351	8	ADO57848	Rat formy
30	64.5	27.4	742	8	ABU20797	Protein e
31	63.5	27.0	935	8	ADU29071	Mouse nov
32	63	26.8	61	4	AAU53825	Propionib
33	63	26.8	61	6	ABM50344	Propionib
34	63	26.8	365	2	AAV43138	Human NAI
35	63	26.8	365	4	AAW23942	Human EST
36	63	26.8	365	5	AAU11929	Human pro
37	63	26.8	365	8	ADP56168	Human PRO
38	63	26.8	365	8	ADP25183	PRO poly
39	63	26.8	368	3	AAW02827	Human G p
40	63	26.8	368	3	AAW19523	G protein
41	63	26.8	368	3	AAW71293	Human orp
42	63	26.8	368	4	AAW70142	Human G p
43	63	26.8	368	4	AAW64288	Human G p
44	63	26.8	368	4	AAU10303	G-protein
45	63	26.8	368	5	AAE19359	Human G-p

ALIGNMENTS

RESULT 1  
AAW73409  
ID AAW73409 standard; protein; 114 AA.  
XX AC AAW73409;  
XX AC AAW73409;  
DT 19-FEB-1999 (first entry)  
DE Human secreted protein encoded by Gene No. 13.  
XX  
KW Secreted protein; human; protein therapy; gene therapy; blood disorder;  
KW pathological condition; diagnosis; cancer; neurological disorder;  
KW developmental abnormality; foetal deficiency; leukaemia; hepatic disease;  
KW immune system disorder; Alzheimer's disease; cognitive disorder;  
KW schizophrenia; prostate disease; autoimmune disorder; AIDS.  
XX Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 114  
FT Misc-difference 114  
FT Misc-difference 114  
XX WO9854206-A1.  
XX  
XX 03-DEC-1998.  
XX 28-MAY-1998; 98WO-US010868.  
XX  
XX 30-MAY-1997; 97US-0044039P.  
XX 30-MAY-1997; 97US-0048093P.  
XX 30-MAY-1997; 97US-0048101P.  
XX 30-MAY-1997; 97US-0048190P.  
XX 30-MAY-1997; 97US-0048356P.  
XX 30-MAY-1997; 97US-0050935P.  
XX 29-AUG-1997; 97US-0056250P.  
XX 29-AUG-1997; 97US-0056293P.  
XX 29-AUG-1997; 97US-0056296P.  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Ruben SM, Rosen CA, Carter KC, Dillon PJ, Endress GA, Yu G;  
XX Ni J, Feng P;  
XX WPI, 1999-070209/06.  
XX N-PSDB; AAW08823.  
XX  
XX New isolated human genes - useful for diagnosis and treatment of, e.g.  
XX cancers, neurological disorders, immune diseases, developmental disorders  
XX

PT or blood disorders.  
XX  
PS Claim 11; Page 153; 189pp; English.  
XX  
CC This sequence is encoded by a cDNA of the invention, designated Gene No.  
CC 13. This sequence represents a human secreted protein, and is expressed  
CC in keratinocytes and to a lesser extent in endothelial cells and  
CC placenta. The DNA sequences of the invention and their corresponding  
CC secreted polypeptides are useful for preventing, treating or ameliorating  
CC medical conditions, e.g. by protein or gene therapy. Also pathological  
CC conditions can be diagnosed by determining the amount of the new  
CC polypeptides in a sample or by determining the presence of mutations in  
CC the DNA sequences. Specific uses are described for each of the DNA  
CC sequences and the encoded proteins, based on which tissues they are most  
CC highly expressed in, and include developing products for the diagnosis or  
CC treatment of cancer, tumours, neurological disorders, developmental  
CC abnormalities and foetal deficiencies, blood disorders, leukaemias,  
CC diseases of the immune system (including allergies or asthma), hepatic  
CC diseases, Alzheimer's and cognitive disorders, schizophrenia, prostate  
CC diseases, autoimmune disorders and AIDS. The polypeptides are also useful  
CC for identifying their binding partners  
XX  
SQ Sequence 114 AA;  
Query Match 100.0%; Score 235; DB 2; Length 114;  
Best Local Similarity 100.0%; Pred. No. 7.1e-23;  
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 PPAPFRLWPILGGALSTFVLGSLGFLVWRCRRSSPPPX 44  
DB 71 PPAPFRLWPILGGALSTFVLGSLGFLVWRCRRSSPPPX 114  
RESULT 2  
ABU64233  
ID ABU64233 standard; protein; 94 AA.  
XX  
AC ABU64233;  
XX  
DT 11-MAR-2004 (first entry)  
XX  
DE Human CRYPTIC protein.  
XX  
KW Metabolic disorder; TNF receptor family member; FRADJ; CRYPTIC; agonist;  
KW antagonist; gene therapy; vaccine; anorectic; cytostatic; anti-HIV;  
KW antiinflammatory; cardiant; ophthalmological; neuroprotective;  
KW nephrotropic; antidiabetic; antiarteriosclerotic; hypotensive;  
KW antilipemic; weight loss; obesity; diabetes.  
XX  
OS Homo sapiens.  
XX  
FN WO2003077939-A1.  
XX  
PD 25-SEP-2003.  
XX  
PF 17-MAR-2003; 2003WO-EP050066.  
XX  
PR 19-MAR-2002; 2002US-0365851P.  
PR 14-MAY-2002; 2002US-0380565P.  
XX  
FA (GEST ) GENSET SA.  
XX  
PI Dialynas D, Lucas J, Scalia A;  
XX  
DR WPI; 2003-779086/73.  
DR N-PSDB; NAL56187.  
XX  
XX Use of FRADJ or CRYPTIC polypeptide for preparing a medicament for  
PT treating or preventing a disorder associated with excessive weight loss  
PT or an obesity-related disorder.  
XX  
XX Claim 2; Page 201; 206pp; English.  
PS  
XX

CC The present invention provides the human FRADJ and CRYPTIC proteins.  
CC These can be used in screening for antagonists or agonists of APM1  
CC polypeptide or polypeptide fragment activity, comprising lipid  
CC partitioning, lipid metabolism or insulin-like activity. The agonist or  
CC antagonist of FRADJ or CRYPTIC is useful for preparing a medicament for  
CC treating or preventing a disorder associated with excessive weight loss,  
CC comprising cachexia, cancer-related weight loss, AIDS-related weight  
CC loss, chronic inflammatory disease-related weight loss, bulimia or  
CC anorexia, or an obesity-related disorder, comprising obesity, insulin  
CC resistance, atherosclerosis, atheromatous disease, heart disease,  
CC hypertension, stroke, syndrome x, insulin or non-insulin dependent  
CC diabetes mellitus, hyperlipidaemia, hyperuricaemia or diabetes-related  
CC complications, e.g., microangiopathic lesions, ocular lesions,  
CC retinopathy, neuropathy or renal lesions. The present sequence is a  
CC polypeptide shown in the exemplification of the invention  
XX  
SQ Sequence 94 AA;  
Query Match 84.7%; Score 199; DB 7; Length 94;  
Best Local Similarity 84.1%; Pred. No. 3.1e-18;  
Matches 37; Conservative 1; Mismatches 6; Indels 0; Gaps 0;  
QY 1 PPAPFRLWPILGGALSTFVLGSLGFLVWRCRRSSPPPX 44  
DB 36 PPAPFRLWPILGGALSTFVLGSLGFLVWRCRRREKFTTPI 79  
RESULT 3  
AAW88506  
ID AAW88506 standard; protein; 129 AA.  
XX  
AC AAW88506;  
XX  
DT 30-MAR-1999 (first entry)  
XX  
DE Human liver clone HP10432-encoded membrane protein.  
XX  
KW Transmembrane protein; HP10432; human; liver.  
XX  
OS Homo sapiens.  
XX  
FN WO9855508-A2.  
XX  
PD 10-DEC-1998.  
XX  
PF 03-JUN-1998; 98WO-JP002445.  
XX  
PR 03-JUN-1997; 97JP-0014948.  
XX  
PA (SAGA ) SAGAMI CHEM RES CENTRE.  
PA (PROT-) PROTEGENE INC.  
XX  
PI Kato S, Sekine S, Yamaguchi T;  
XX  
DR WPI; 1999-045730/04.  
DR N-PSDB; AAV84374.  
XX  
PT New human proteins containing transmembrane domains and their encoding  
PT sequences - useful in the preparation of antibodies and large-scale  
PT protein production, gene diagnosis, and gene therapy.  
XX  
PS Claim 1; Page 152-153; 178pp; English.  
XX  
CC This is the amino acid sequence of a transmembrane protein encoded by  
CC human liver cDNA clone HP10432 (see AAV84374). The encoded protein has a  
CC signal-like N-terminal region and one internal transmembrane domain. The  
CC invention provides nucleotide sequences (see AAV84359-76) coding for 18  
CC transmembrane proteins (see AAW8491-508), vectors containing such  
CC polynucleotides, and eukaryotic cells containing the vectors. The  
CC proteins can be used as antigens or as compositions in the preparation of  
CC antibodies against the proteins. The polynucleotides can be used as  
CC probes for gene diagnosis, and as gene sources for gene therapy and large  
CC scale production of proteins encoded by the cDNA. The host cells are

CC used for the detection of ligands corresponding to the expressed  
 CC proteins, and the screening of low mol.wt. medicines

SQ Sequence 129 AA;

Query Match 84.7%; Score 199; DB 2; Length 129;  
 Best Local Similarity 84.1%; Pred. No. 4.3e-18;  
 Matches 37; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PPAPFRLWPILGGALSITFVLGSLGFLVWRCRRERSPPPX 44  
 |||||  
 DB 71 PPAPFRLWPILGGALSITFVLGSLGFLVWRCRRREKFTTPI 114  
 |||||

#### RESULT 4

AAV57940  
 ID AAV57940 standard; protein; 129 AA.

XX AC AAV57940;

DT 23-MAR-2000 (first entry)

DE Human transmembrane protein HTPPN-64.

XX Human; transmembrane protein; HTPPN; diagnosis; immunospecific;  
 KW antiproliferative; neuroprotective; immune disorder;  
 KW reproductive disorder; smooth muscle disorder; neurological disorder;  
 KW gastrointestinal disorder; developmental disorder;  
 KW cell proliferative disorder.

XX OS Homo sapiens.

XX FH WO9961471-A2.

XX PD 02-DEC-1999.

XX PF 28-MAY-1999; 99WO-US011904.

XX PR 29-MAY-1998; 98US-0087260P.

XX PR 02-JUL-1998; 98US-0091674P.

XX PR 02-OCT-1998; 98US-0102954P.

XX PR 24-NOV-1998; 98US-0109869P.

XX PA (INCY-) INCYTE PHARM INC.

XX PI Tang YT, Lal P, Hillman JL, Yue H, Guegler KJ, Corley NC;

PI Bandman O, Patterson C, Gorgone GA, Kaser MR, Baughn MR, Au-Young J;

XX DR WPI; 2000-072605/06.

XX DR N-PSDB; AAZ56761.

XX PT Proteins, polynucleotides, vectors, host cells and antibodies used to  
 PT diagnose, treat or prevent immune, reproductive, smooth muscle,  
 PT neurological, gastrointestinal, developmental and cell proliferative  
 PT disorders.

XX PS Claim 1; Page 163; 229pp; English.

XX CC AAZ56698 to AAZ56776 encode AAV57877 to AAV57955 which represent human  
 CC transmembrane proteins designated HTPPN-1 to HTPPN-79, respectively. The  
 CC transmembrane protein have immunospecific, antiproliferative and  
 CC neuroprotective activities. The human transmembrane proteins,  
 CC polynucleotides encoding them and other compositions and methods from the  
 CC present invention, can be used for the diagnosis, treatment or prevention  
 CC of immune, reproductive, smooth muscle, neurological, gastrointestinal,  
 CC developmental and cell proliferative disorders. The HTPPN's can be used  
 CC to treat or prevent disorders associated with a decreased expression or  
 CC activity of HTPPN

XX SQ Sequence 129 AA;

Query Match 84.7%; Score 199; DB 3; Length 129;  
 Best Local Similarity 84.1%; Pred. No. 4.3e-18;

Matches 37; Conservative 1; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 PPAPFRLWPILGGALSITFVLGSLGFLVWRCRRERSPPPX 44  
 |||||  
 DB 71 PPAPFRLWPILGGALSITFVLGSLGFLVWRCRRREKFTTPI 114  
 |||||

#### RESULT 5

AAU03498  
 ID AAU03498 standard; protein; 129 AA.

XX AC AAU03498;

XX DT 26-SEP-2001 (first entry)

XX DE Human TWEAK receptor (TWEAKR) polypeptide.

XX KW TWEAK receptor; TWEAKR; tumour necrosis factor; TNF; angiogenesis;  
 KW ocular neovascularisation; diabetic retinopathy; neovascular glaucoma;  
 KW retinoblastoma; retinopathy of prematurity; retrolental fibroplasia;  
 KW rubrosis; uveitis; macular degeneration; arthritis; rheumatism;  
 KW corneal graft neovascularisation; psoriasis; metastatic condition;  
 KW malignant tumour; sarcoma; carcinoma; benign tumour; haemophilic joint;  
 KW preneoplastic condition; myocardial angiogenesis; wound granulation;  
 KW scleroderma; vascular adhesion; telangiectasia; ischaemia; human;  
 KW atherosclerotic plaque neovascularisation; coronary atherosclerosis;  
 KW peripheral atherosclerosis.

XX OS Homo sapiens.

XX FH WO200145730-A2.

XX PD 28-JUN-2001.

XX PF 19-DEC-2000; 2000WO-US034755.

XX PR 20-DEC-1999; 99US-0172878P.

XX PR 10-MAY-2000; 2000US-0203347P.

XX PA (IMMV) IMMUNEX CORP.

XX PI Wiley SR;

XX DR WPI; 2001-417975/44.

XX DR N-PSDB; AAS03963.

XX PT Modulating angiogenesis in a mammal for treating diseases mediated by  
 PT angiogenesis, e.g. solid tumors and vascular deficiencies of cardiac or  
 PT peripheral tissue, by administering antagonist or agonist of TWEAK  
 PT receptor.

XX PS Example 1; Fig 1; 46pp; English.

XX CC The sequence represents the human TWEAK receptor (TWEAKR) protein. The  
 CC TWEAK protein is a member of the tumour necrosis factor (TNF) family and  
 CC induces angiogenesis. TWEAKR may therefore be used to screen for and  
 CC develop TWEAKR agonists and antagonists for the modulation of  
 CC angiogenesis, to be used in the treatment and diagnosis of human disease.  
 CC The disorders mediated by angiogenesis include ocular disorders  
 CC characterised by ocular neovascularisation such as diabetic retinopathy,  
 CC neovascular glaucoma, retinoblastoma, retinopathy of prematurity,

CC retrolental fibroplasia, rubeosis, uveitis, macular degeneration and  
 CC corneal graft neovascularisation, and inflammatory diseases such as  
 CC arthritis, rheumatism and psoriasis. Other treatable diseases include  
 CC malignant and metastatic conditions such as sarcomas and carcinomas,  
 CC benign tumours and preneoplastic conditions, myocardial angiogenesis,  
 CC haemophilic joints, scleroderma, vascular adhesions, atherosclerotic  
 CC plaque neovascularisation, telangiectasia, wound granulation, coronary  
 CC atherosclerosis, peripheral atherosclerosis and ischaemia  
 XX  
 SQ Sequence 129 AA;

Query Match 84.7%; Score 199; DB 4; Length 129;  
 Best Local Similarity 84.1%; Pred. No. 4.3e-18;  
 Matches 37; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PPAPFRLWPILGGALSITFVLGSLGFLVWRCRRSSPPPX 44  
 |||||  
 DB 71 PPAPFRLWPILGGALSITFVLGSLGFLVWRCRRREKFTTPI 114  
 |||||

RESULT 6  
 ABP61512  
 ID ABP61512 standard; protein; 129 AA.  
 XX  
 AC ABP61512;  
 XX  
 DT 30-SEP-2002 (first entry)  
 XX  
 DE Human NF-KB activating protein SEQ ID NO 178.  
 XX  
 KW Human; NF-kB; nuclear factor kappa B; mouse; antiinflammatory;  
 KW immunomodulator; cytostatic; antineoplastic; osteopathic; neotropic;  
 KW neuroprotective; anti-HIV; autoimmune disease; cancer; infection;  
 KW bone disease; AIDS; neurodegenerative disease; ischaemic disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200253737-A1.  
 XX  
 PD 11-JUL-2002.  
 XX  
 PF 25-DEC-2001; 2001WO-JP011389.  
 XX  
 PR 28-DEC-2000; 2000JP-00402288.  
 PR 26-MAR-2001; 2001JP-00088912.  
 PR 24-AUG-2001; 2001JP-00254018.  
 XX  
 PA (ASAH ) ASAH KASEI KOGYO KK.  
 XX  
 PI Matsuda A, Honda G, Muramatsu S, Nagano Y;  
 XX  
 DR WPI; 2002-583617/62.  
 DR N-PSDB; ABQ92000.  
 XX  
 PT NF-approximatelykB activating gene and expressed protein, applicable in  
 PT diagnosis and screening inhibitors or promoters to control excessive  
 PT activation or inhibition for treating e.g. inflammations, autoimmune  
 PT diseases and cancer.  
 XX  
 PS Claim 4; Page 814-815; 841pp; Japanese.  
 XX  
 CC The invention relates to a purified protein (I), comprising one of 90  
 CC fully defined sequences (ABP61424-ABP61513) or a protein based on any of  
 CC the sequences but with some amino acids deleted, substituted or added and  
 CC with a NF-kB (nuclear factor kappa B) activating effect. The protein and  
 CC encoding gene (ABQ91912-ABQ92001) are useful in diagnosis and screening  
 CC inhibitors or promoters to control excessive activation or inhibition and  
 CC for treating e.g. inflammations, autoimmune diseases, cancers,  
 CC infections, bone diseases, AIDS, neurodegenerative diseases or ischaemic  
 CC disorders  
 XX  
 SQ Sequence 129 AA;

Query Match 84.7%; Score 199; DB 5; Length 129;  
 Best Local Similarity 84.1%; Pred. No. 4.3e-18;  
 Matches 37; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PPAPFRLWPILGGALSITFVLGSLGFLVWRCRRSSPPPX 44  
 |||||  
 DB 71 PPAPFRLWPILGGALSITFVLGSLGFLVWRCRRREKFTTPI 114  
 |||||

RESULT 7  
 AAU79827  
 ID AAU79827 standard; protein; 129 AA.  
 XX  
 AC AAU79827;  
 XX  
 DT 15-JUL-2002 (first entry)  
 XX  
 DE Human type 1 transmembrane protein Fn14.  
 XX  
 KW Type 1 transmembrane protein Fn14; human; cytostatic; cardiant;  
 KW vulnery; TWEAK agonist; Fn14 agonist; angiogenesis; tumour progression;  
 KW tumour necrosis factor family; TNF family; TWEAK receptor;  
 KW myocardial ischaemic condition; myocardial infarction; wound healing;  
 KW burn healing; gastric ulcer; tissue transplantation;  
 KW organ transplantation; neovascularisation; vascular insufficiency;  
 KW cancer; inflammatory macular degeneration; diabetic retinopathy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200222166-A2.  
 XX  
 PD 21-MAR-2002.  
 XX  
 PF 12-SEP-2001; 2001WO-US028451.  
 XX  
 PR 14-SEP-2000; 2000US-0232355P.  
 XX  
 PA (BIOJ ) BIOGEN INC.  
 XX  
 PI Browning J, Burkly L, Jakubowski A, Zheng T;  
 XX  
 DR WPI; 2002-383103/41.  
 XX  
 PT Methods of modulating angiogenesis and inhibiting tumor progression,  
 PT using TWEAK receptor agonists.  
 XX  
 PS Disclosure; Fig 10A; 37pp; English.  
 XX  
 CC The invention describes methods of modulating angiogenesis and inhibiting  
 CC tumour progression using TWEAK (a novel member of the tumour necrosis  
 CC factor or TNF family) receptor agonists. Conditions which can be treated  
 CC using the agonists include myocardial ischaemic conditions (e.g.  
 CC myocardial infarction), wound healing (e.g. burn healing and healing of  
 CC gastric ulcers), and tissue and organ transplantations to promote  
 CC neovascularisation, particularly in subjects suffering from vascular  
 CC insufficiency (e.g. diabetic patients). Inhibition of angiogenesis and  
 CC subsequently neovascularisation is useful in treatment of cancer,  
 CC inflammatory macular degeneration and diabetic retinopathy. This sequence  
 CC represents the human type 1 transmembrane protein Fn14, a TWEAK receptor  
 CC described in the invention  
 XX  
 SQ Sequence 129 AA;

Query Match 84.7%; Score 199; DB 5; Length 129;  
 Best Local Similarity 84.1%; Pred. No. 4.3e-18;  
 Matches 37; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PPAPFRLWPILGGALSITFVLGSLGFLVWRCRRSSPPPX 44  
 |||||  
 DB 71 PPAPFRLWPILGGALSITFVLGSLGFLVWRCRRREKFTTPI 114  
 |||||

RESULT 8

CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 129 AA;  
  
Query Match 84.7%; Score 199; DB 6; Length 129;  
Best Local Similarity 84.1%; Pred. No. 4.3e-18;  
Matches 37; Conservative 1; Mismatches 6; Indels 0; Gaps 0  
  
Qy 1 PPAPFLLWPIILGALSLTFVLGSLGFLVWRRCRRERSPPPX 44  
|||||  
Db 71 PPAPFLLWPIILGALSLTFVLGSLGFLVWRRCRRERKFTTPI 114  
|||||  
  
RESULT 9  
ABUS6716  
ID ABUS6716 standard; protein; 129 AA.  
XX  
AC ABUS6716;  
XX  
DT 02-APR-2003 (first entry)  
XX  
XX  
DB Lung cancer-associated polypeptide #309.  
XX  
XX Lung cancer-associated polypeptide; cytostatic; emphysema;  
KW antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;  
KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;  
KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;  
KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.  
XX  
OS Unidentified.  
XX  
FN WO200286443-A2.  
XX  
PD 31-OCT-2002.  
XX  
PF 18-APR-2002; 2002WO-US012476.  
XX  
PR 18-APR-2001; 2001US-0284770P.  
PR 10-MAY-2001; 2001US-0290492P.  
PR 09-NOV-2001; 2001US-0339245P.  
PR 13-NOV-2001; 2001US-0350666P.  
PR 29-NOV-2001; 2001US-0334370P.  
PR 12-APR-2002; 2002US-0372246P.  
XX  
PS (EOSB-) EOS BIOTECHNOLOGY INC.  
XX  
PI Aziz N, Murray R;  
XX  
DR WPI; 2003-093161/08.  
XX N-PSDB; ABX76445.  
XX  
PT Detecting a lung cancer-associated transcript in a cell from a patient  
PT for treating lung cancer, by contacting a biological sample from the  
PT patient with a polynucleotide that exhibits increased or decreased  
PT expression in lung cancer.  
XX  
PS Claim 27; Page 429; 453pp; English.  
XX  
CC The invention relates to a method for detecting a lung cancer-associated  
CC transcript in a cell from a patient, comprising contacting a biological  
CC sample from the patient with a polynucleotide that selectively hybridises  
CC to a sequence that is at least 80 % identical to a gene that exhibits  
CC increased or decreased expression in lung cancer samples. Lung cancer-  
CC associated polynucleotides and polypeptides are used for identifying a  
CC compound that modulates a lung cancer-associated polypeptide, for  
CC inhibiting proliferation of a lung cancer-associated cell to treat lung  
CC cancer in a patient and for treating a mammal having lung cancer by  
CC administering a modulatory compound identified. The methods are useful  
CC for treating lung cancer, such as small cell lung cancer, non-small cell  
CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,  
CC emphysema, bronchitis chronic obstructive pulmonary disease, fibrosis,  
CC hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and  
CC bronchiectasis. The genes, polynucleotides and polypeptides are useful  
CC



CC immunological probes for differential identification of the tissues  
CC immunohistochemistry assays. The present sequence represents a human  
CC secreted protein.  
XX  
XX  
SQ Sequence 129 AA;

Query Match 84.7%; Score 199; DB 7; Length 129;  
Best Local Similarity 84.1%; Pred. No. 4.3e-18;  
Matches 37; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PPAPFRLWPILGGALSLTFVLGSLGFLVWRCRRSSPPPX 44  
|||  
DB 71 PPAPFRLWPILGGALSLTFVLGSLGFLVWRCRRREKFTTPI 114  
|||

## RESULT 12

ADD89033  
ID ADD89033 standard; protein; 129 AA.

AC ADD89033;

XX 29-JAN-2004 (first entry)

XX TAT274.

XX tumour-associated antigenic target polypeptide; Cytostatic; tumour;  
KW cancer.

XX Homo sapiens.

XX WO2003057160-A2.

XX 17-JUL-2003.

XX 30-DEC-2002; 2002WO-US041798.

XX 02-JAN-2002; 2002US-0345444P.

XX 25-JAN-2002; 2002US-0351885P.

XX 25-FEB-2002; 2002US-0360066P.

XX 05-MAR-2002; 2002US-0362004P.

XX 20-MAR-2002; 2002US-0366869P.

XX 21-MAR-2002; 2002US-0366284P.

XX 28-MAR-2002; 2002US-0368679P.

XX 19-AUG-2002; 2002US-0404809P.

XX 21-AUG-2002; 2002US-0405645P.

XX (GETH ) GENENTECH INC.

XX Frantz G, Hillan KJ, Phillips H, Polakis P, Smith V, Spencer SD;  
PI Williams PM, Wu TD, Zhang Z;  
XX  
XX WPI: 2003-569537/53.  
XX N-PSDB; ADD89109.

XX New antibodies against tumor-associated antigenic target polypeptide,  
PT useful for treating or diagnosing tumors or cancers in mammals, e.g.  
PT prostate cancer, lung cancer, prostate adenocarcinomas or renal cell  
PT carcinomas.

XX Claim 1; SEQ ID NO 37; 252pp; English.  
XX The present invention relates to antibodies against tumour-associated  
CC antigenic target polypeptide. The antibody is useful for treating or  
CC diagnosing tumors or cancers in mammals, e.g. prostate cancer, lung  
CC cancer, breast cancer, colon cancer, ovarian cancer, prostate  
CC adenocarcinomas, renal cell carcinomas, or pleural mesothelioma. The  
CC present sequence represents a TAT polypeptide.

XX Sequence 129 AA;

Query Match 84.7%; Score 199; DB 7; Length 129;  
Best Local Similarity 84.1%; Pred. No. 4.3e-18;  
Matches 37; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PPAPFRLWPILGGALSLTFVLGSLGFLVWRCRRSSPPPX 44  
|||  
DB 71 PPAPFRLWPILGGALSLTFVLGSLGFLVWRCRRREKFTTPI 114  
|||

## RESULT 13

ABU64232

XX ABU64232 standard; protein; 129 AA.

XX AC ABU64232;

XX 11-MAR-2004 (first entry)

XX Human FRADJ protein.

XX Metabolic disorder; TNF receptor family member; FRADJ; CRYPTIC; agonist;  
KW antagonist; gene therapy; vaccine; anorectic; cytostatic; anti-HIV;  
KW antiinflammatory; cardiatic; ophthalmological; neuroprotective;  
KW nephrotropic; antidiabetic; antiarteriosclerotic; hypotensive;  
KW antilipemic; weight loss; obesity; diabetes.

XX Homo sapiens.

XX WO2003077939-A1.

XX 25-SEP-2003.

XX 17-MAR-2003; 2003WO-EP050066.

XX 19-MAR-2002; 2002US-0365851P.

XX 14-MAY-2002; 2002US-0380565P.

XX (GEST ) GENSET SA.

XX Dialynas D, Lucas J, Scalia A;

XX WPI: 2003-779086/73.

XX N-PSDB; AAL56186.

XX Use of FRADJ or CRYPTIC polypeptide for preparing a medicament for loss  
PT treating or preventing a disorder associated with excessive weight loss  
XX or an obesity-related disorder.

XX Claim 1; Page 200; 206pp; English.

XX The present invention provides the human FRADJ and CRYPTIC proteins.  
CC These can be used in screening for antagonists or agonists of APM1  
CC polypeptide or polypeptide fragment activity, comprising lipid  
CC partitioning, lipid metabolism or insulin-like activity. The agonist or  
CC antagonist of FRADJ or CRYPTIC is useful for preparing a medicament for  
CC treating or preventing a disorder associated with excessive weight loss,  
CC comprising cachexia, cancer-related weight loss, AIDS-related weight  
CC loss, chronic inflammatory disease-related weight loss, bulimia or  
CC anorexia, or an obesity-related disorder, comprising obesity, insulin  
CC resistance, atherosclerosis, atheromatous disease, heart disease,  
CC hypertension, stroke, syndrome x, insulin or non-insulin dependent  
CC diabetes mellitus, hyperlipidaemia, hyperuricaemia or diabetes-related  
CC complications, e.g., microangiopathic lesions, ocular lesions, is a  
CC retinopathy, neuropathy or renal lesions. The present sequence is a  
CC polypeptide shown in the exemplification of the invention

XX Sequence 129 AA;

Query Match 84.7%; Score 199; DB 7; Length 129;  
Best Local Similarity 84.1%; Pred. No. 4.3e-18;  
Matches 37; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PPAPFRLWPILGGALSLTFVLGSLGFLVWRCRRSSPPPX 44  
|||  
DB 71 PPAPFRLWPILGGALSLTFVLGSLGFLVWRCRRREKFTTPI 114  
|||

RESULT 14  
ADN39126  
ID ADN39126 standard; protein; 129 AA.  
XX  
XX ADN39126;  
XX AC  
XX DT 17-JUN-2004 (first entry)  
XX DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:444.  
XX KW Human; differential expression; cancer; angiogenic disorder;  
KW fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;  
KW inflammatory disease; autoimmune disease;  
KW retinal neovascularisation syndrome; scarring; uterine fibroid;  
KW detection; diagnosis; prognosis; drug screening; drug targeting;  
KW wound healing; contraception; cytostatic; cardiant; immunomodulatory;  
KW vulnery; gene therapy; vaccine.  
XX OS Homo sapiens.  
XX PN WO2003042661-A2.  
XX PD 22-MAY-2003.  
XX PF 13-NOV-2002; 2002WO-US036810.  
XX PR 13-NOV-2001; 2001US-0350666P.  
XX PR 21-NOV-2001; 2001US-0332464P.  
XX PR 29-NOV-2001; 2001US-0334393P.  
XX PR 03-DEC-2001; 2001US-0335394P.  
XX PR 14-DEC-2001; 2001US-0340376P.  
XX PR 08-JAN-2002; 2002US-0347211P.  
XX PR 10-JAN-2002; 2002US-0347349P.  
XX PR 08-FEB-2002; 2002US-035250P.  
XX PR 13-FEB-2002; 2002US-0356714P.  
XX PR 20-FEB-2002; 2002US-0359077P.  
XX PR 29-MAR-2002; 2002US-036809P.  
XX PR 12-APR-2002; 2002US-0370110P.  
XX PR 29-MAR-2002; 2002US-036809P.  
XX PR 04-APR-2002; 2002US-0370110P.  
XX PR 05-JUN-2002; 2002US-0386614P.  
XX PR 16-JUL-2002; 2002US-0396839P.  
XX PR 22-JUL-2002; 2002US-0397775P.  
XX PR 22-JUL-2002; 2002US-0397845P.  
XX PR 09-SEP-2002; 2002US-0409450P.  
XX PA (EOSB-) EOS BIOTECHNOLOGY INC.  
XX PI Afar D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Hevezi PA;  
PI Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;  
XX WPI; 2003-468649/44.  
XX DR N-PSDB; ADN39125.  
XX PT Determining the presence or absence of a pathological cell in a patient,  
XX useful for diagnosing, prognosing or treating cancer, comprises detecting  
XX a nucleic acid in a biological sample.  
XX PS Claim 12; SEQ ID NO 444; 1385pp; English.  
XX CC The invention relates to nucleic acids and proteins (ADN38683-ADN40064)  
CC whose expression is upregulated or downregulated in specific cancers or  
CC other diseases such as angiogenic or fibrotic disorders, and to methods  
CC of determining the presence or absence of a pathological cell in a  
CC patient by detecting a nucleic acid at least 80% identical to those of  
CC the invention or by detecting a polypeptide of the invention. The  
CC invention also relates to expression vectors and host cells comprising a  
CC nucleic acid of the invention; antibodies which specifically bind a  
CC polypeptide of the invention; use of such antibodies for drug targeting;  
CC and methods of screening for modulators of activity or expression of the  
CC polypeptides and nucleic acids. The nucleic acids, polypeptides, and  
CC antibodies and methods are useful for diagnosing, prognosing and treating  
CC cancer and other conditions such as psoriasis, ischaemia, heart disease,  
CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal

CC neovascularisation syndromes, scarring and uterine fibroids. They may  
CC also be useful in wound healing and in contraception. The present  
CC sequence represents a polypeptide of the invention.  
XX  
XX SQ Sequence 129 AA;  
Query Match 84.7%; Score 199; DB 7; Length 129;  
Best Local Similarity 84.1%; Pred. No. 4.3e-18;  
Matches 37; Conservative 1; Mismatches 6; Indels 0; Gaps 0;  
QY 1 PPAPRLLPILGGLSLTFLVGLSGFLVWRCRRSSPPX 44  
DB 71 PPAPRLLPILGGLSLTFLVGLSGFLVWRCRRREKFTTPI 114  
RESULT 15  
ADN39987  
ID ADN39987 standard; protein; 129 AA.  
XX  
XX AC ADN39987;  
XX DT 17-JUN-2004 (first entry)  
XX DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO: C357.  
XX KW Human; differential expression; cancer; angiogenic disorder;  
KW fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;  
KW inflammatory disease; autoimmune disease;  
KW retinal neovascularisation syndrome; scarring; uterine fibroid;  
KW detection; diagnosis; prognosis; drug screening; drug targeting;  
KW wound healing; contraception; cytostatic; cardiant; immunomodulatory;  
KW vulnery; gene therapy; vaccine.  
XX OS Homo sapiens.  
XX PN WO2003042661-A2.  
XX PD 22-MAY-2003.  
XX PF 13-NOV-2002; 2002WO-US036810.  
XX PR 13-NOV-2001; 2001US-0350666P.  
XX PR 21-NOV-2001; 2001US-0332464P.  
XX PR 29-NOV-2001; 2001US-0334393P.  
XX PR 03-DEC-2001; 2001US-0335394P.  
XX PR 14-DEC-2001; 2001US-0340376P.  
XX PR 08-JAN-2002; 2002US-0347211P.  
XX PR 10-JAN-2002; 2002US-0347349P.  
XX PR 08-FEB-2002; 2002US-035250P.  
XX PR 13-FEB-2002; 2002US-0356714P.  
XX PR 20-FEB-2002; 2002US-0359077P.  
XX PR 29-MAR-2002; 2002US-036809P.  
XX PR 12-APR-2002; 2002US-0370110P.  
XX PR 29-MAR-2002; 2002US-036809P.  
XX PR 04-APR-2002; 2002US-0370110P.  
XX PR 05-JUN-2002; 2002US-0386614P.  
XX PR 16-JUL-2002; 2002US-0396839P.  
XX PR 22-JUL-2002; 2002US-0397775P.  
XX PR 22-JUL-2002; 2002US-0397845P.  
XX PR 09-SEP-2002; 2002US-0409450P.  
XX PA (EOSB-) EOS BIOTECHNOLOGY INC.  
XX PI Afar D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Hevezi PA;  
PI Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;  
XX WPI; 2003-468649/44.  
XX DR N-PSDB; ADN39970.  
XX PT Determining the presence or absence of a pathological cell in a patient,  
XX useful for diagnosing, prognosing or treating cancer, comprises detecting  
XX a nucleic acid in a biological sample.  
XX PS Claim 12; SEQ ID NO C357; 1385pp; English.





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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 14, 2005, 07:23:28 ; Search time 130 Seconds  
(without alignments)  
110.592 Million cell updates/sec

Title: US-10-062-831-59\_COPY\_71\_114

Perfect score: 235

Sequence: 1 PPAPRLLPILGGALSLTF.....LSGFLVRRRRSSPPPX 44

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 1376875 seqs, 326749119 residues

Total number of hits satisfying chosen parameters: 1376875

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US05\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09D\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/2/pubpaa/US09E\_PUBCOMB.pep:\*
- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*
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- 16: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep:\*
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- 18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*
- 19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*
- 20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	235	100.0	114	14	US-10-062-599-59
3	199	84.7	129	9	US-09-742-454A-4
4	199	84.7	129	9	US-09-883-777-4
5	199	84.7	129	14	US-10-024-238A-178
6	199	84.7	129	14	US-10-042-211A-178
7	199	84.7	129	15	US-10-331-496A-37
8	199	84.7	129	15	US-10-295-027-444
9	199	84.7	129	15	US-10-295-027-1305
10	199	84.7	129	15	US-10-617-217A-178
11	164	69.8	129	9	US-09-742-454A-5
12	164	69.8	129	9	US-09-883-777-5
13	67	28.5	426	15	US-10-257-174-44

Sequence 6, Appli  
Sequence 48721, A  
Sequence 5, Appli  
Sequence 59, Appli  
Sequence 2, Appli  
Sequence 6, Appli  
Sequence 627, App  
Sequence 6, Appli  
Sequence 4, Appli  
Sequence 6, Appli  
Sequence 3, Appli  
Sequence 6, Appli  
Sequence 60, Appli  
Sequence 6, Appli  
Sequence 6, Appli  
Sequence 2579, Ap  
Sequence 2, Appli  
Sequence 154909,  
Sequence 454, App  
Sequence 56, Appli  
Sequence 8, Appli  
Sequence 17, Appli  
Sequence 19, Appli  
Sequence 8, Appli  
Sequence 175064,  
Sequence 4, Appli  
Sequence 4, Appli  
Sequence 4, Appli  
Sequence 177016,  
Sequence 47140, A

#### ALIGNMENTS

RESULT 1  
US-10-062-831-59  
; Sequence 59, Application US/10062831  
; Publication No. US20030105297A1  
; GENERAL INFORMATION:  
; APPLICANT: Steven M. Ruben, et al.  
; TITLE OF INVENTION: 32 Human Secreted Proteins  
; FILE REFERENCE: PZ006P1  
; CURRENT APPLICATION NUMBER: US/10/062.831  
; CURRENT FILING DATE: 2002-02-05  
; PRIOR APPLICATION NUMBER: 09/690,454  
; PRIOR FILING DATE: 1998-11-10  
; PRIOR APPLICATION NUMBER: PCT/US98/10868  
; PRIOR FILING DATE: May 28, 1998  
; PRIOR APPLICATION NUMBER: 60/044,039  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/048,093  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/048,190  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/050,935  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/048,101  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/048,356  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/056,250  
; PRIOR FILING DATE: August 29, 1997  
; PRIOR APPLICATION NUMBER: 60/056,296  
; PRIOR FILING DATE: August 29, 1997  
; PRIOR APPLICATION NUMBER: 60/056,293  
; PRIOR FILING DATE: August 29, 1997  
; NUMBER OF SEQ ID NOS: 229  
; SOFTWARE: PatentIn ver. 2.0  
; SEQ ID NO 59  
; LENGTH: 114

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; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (114)
; OTHER INFORMATION: Xaa equals stop translation
US-10-062-831-59

Query Match      100.0%; Score 235; DB 14; Length 114;
Best Local Similarity 100.0%; Pred. No. 8.1e-20;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPAPFLLWPILGGALSTFVLGSLGFLVWRCRRSSPPPX 44
    |||||||
Db 71 PPAPFLLWPILGGALSTFVLGSLGFLVWRCRRSSPPPX 114

RESULT 2
US-10-062-599-59
; Sequence 59, Application US/10062599
; Publication No. US20030195346A1
; GENERAL INFORMATION:
; APPLICANT: Steven M. Ruben, et al.
; TITLE OF INVENTION: 32 Human Secreted Proteins
; FILE REFERENCE: PZ006P1
; CURRENT APPLICATION NUMBER: US/10/062,599
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: 09/590,454
; PRIOR FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: 09/189,144
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 60/044,039
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,093
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,190
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/050,935
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,101
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/048,356
; PRIOR FILING DATE: May 30, 1997
; PRIOR APPLICATION NUMBER: 60/056,250
; PRIOR FILING DATE: August 29, 1997
; PRIOR APPLICATION NUMBER: 60/056,296
; PRIOR FILING DATE: August 29, 1997
; PRIOR APPLICATION NUMBER: 60/056,293
; PRIOR FILING DATE: August 29, 1997
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 59
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (114)
; OTHER INFORMATION: Xaa equals stop translation
US-10-062-599-59

Query Match      100.0%; Score 235; DB 14; Length 114;
Best Local Similarity 100.0%; Pred. No. 8.1e-20;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PPAPFLLWPILGGALSTFVLGSLGFLVWRCRRSSPPPX 44
    |||||||
Db 71 PPAPFLLWPILGGALSTFVLGSLGFLVWRCRRSSPPPX 114

RESULT 3
US-09-742-454A-4
; Sequence 4, Application US/09742454A
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; Patent No. US20020041876A1
; GENERAL INFORMATION:
; APPLICANT: WILEY, Steven R.
; TITLE OF INVENTION: TWEAK Receptor
; FILE REFERENCE: 2968-B
; CURRENT APPLICATION NUMBER: US/09/742,454A
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: 60/203,347
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-742-454A-4

Query Match      84.7%; Score 199; DB 9; Length 129;
Best Local Similarity 84.1%; Pred. No. 1.4e-15;
Matches 37; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 PPAPFLLWPILGGALSTFVLGSLGFLVWRCRRSSPPPX 44
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Db 71 PPAPFLLWPILGGALSTFVLGSLGFLVWRCRRREKFTTPI 114

RESULT 4
US-09-883-777-4
; Sequence 4, Application US/09883777
; Patent No. US20020110853A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: TWEAK RECEPTOR
; FILE REFERENCE: 2968-C
; CURRENT APPLICATION NUMBER: US/09/883,777
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: US 60/203,347
; PRIOR FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: PCT/US00/34755
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/742,454
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 129
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-883-777-4

Query Match      84.7%; Score 199; DB 9; Length 129;
Best Local Similarity 84.1%; Pred. No. 1.4e-15;
Matches 37; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 PPAPFLLWPILGGALSTFVLGSLGFLVWRCRRSSPPPX 44
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Db 71 PPAPFLLWPILGGALSTFVLGSLGFLVWRCRRREKFTTPI 114

RESULT 5
US-10-024-298A-178
; Sequence 178, Application US/10024298A
; Publication No. US20030143540A1
; GENERAL INFORMATION:
; APPLICANT: ASAH KASEI KABUSHIKI KAISHA
; APPLICANT: AKIO MATSUDA
; APPLICANT: GOICHI HONDA
; APPLICANT: SHUJI MURAMATSU
; APPLICANT: YUKIKO NAGANO
```

US-10-024-298A-178  
; TITLE OF INVENTION: NF-K B Activating Gene  
; FILE REFERENCE: 1254-0191P  
; CURRENT APPLICATION NUMBER: US/10/024,298A  
; CURRENT FILING DATE: 2003-04-08  
; PRIOR APPLICATION NUMBER: 60/314,385  
; PRIOR FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: 60/278,641  
; PRIOR FILING DATE: 2001-03-26  
; PRIOR APPLICATION NUMBER: 60/258,315  
; PRIOR FILING DATE: 2000-12-28  
; PRIOR APPLICATION NUMBER: JP254018/2001  
; PRIOR FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: JP008912/2001  
; PRIOR FILING DATE: 2001-03-26  
; PRIOR APPLICATION NUMBER: JP402288/2000  
; PRIOR FILING DATE: 2000-12-28  
; NUMBER OF SEQ ID NOS: 182  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 178  
; LENGTH: 129  
; TYPE: PRT  
; ORGANISM: Homo sapiens

Query Match 84.7%; Score 199; DB 14; Length 129;  
Best Local Similarity 84.1%; Pred. No. 1.4e-15;  
Matches 37; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PPAPFLLWPILGGALSLTFVLGSLGFLVWRCRRSSPPPX 44  
DB 71 PPAPFLLWPILGGALSLTFVLGSLGFLVWRCRRREKFTTPI 114

## RESULT 6

US-10-042-211A-178  
; Sequence 178, Application US/10042211A  
; Publication No. US20030170719A1

GENERAL INFORMATION:  
; APPLICANT: MATSUDA, Akio et al.  
; TITLE OF INVENTION: NFkB Activating Gene  
; FILE REFERENCE: 1254-0192P  
; CURRENT APPLICATION NUMBER: US/10/042,211A  
; CURRENT FILING DATE: 2002-01-11  
; PRIOR APPLICATION NUMBER: JP 2000-402288  
; PRIOR FILING DATE: 2000-12-28  
; PRIOR APPLICATION NUMBER: JP 2001-088912  
; PRIOR FILING DATE: 2001-03-26  
; PRIOR APPLICATION NUMBER: JP 2001-254018  
; PRIOR FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: US 60/258,315  
; PRIOR FILING DATE: 2000-12-28  
; PRIOR APPLICATION NUMBER: US 60/278,640  
; PRIOR FILING DATE: 2001-03-26  
; PRIOR APPLICATION NUMBER: US 60/314,385  
; PRIOR FILING DATE: 2001-08-24  
; NUMBER OF SEQ ID NOS: 182  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 178  
; LENGTH: 129  
; TYPE: PRT  
; ORGANISM: Homo sapiens

Query Match 84.7%; Score 199; DB 14; Length 129;  
Best Local Similarity 84.1%; Pred. No. 1.4e-15;  
Matches 37; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PPAPFLLWPILGGALSLTFVLGSLGFLVWRCRRSSPPPX 44  
DB 71 PPAPFLLWPILGGALSLTFVLGSLGFLVWRCRRREKFTTPI 114

## RESULT 7

US-10-331-496A-37  
; Sequence 37, Application US/10331496A  
; Publication No. US20030228305A1  
; GENERAL INFORMATION:  
; APPLICANT: FRANTZ, GRETCHEN  
; APPLICANT: HILLAN, KENNETH J.  
; APPLICANT: PHILLIPS, HEIDI S.  
; APPLICANT: POLAKIS, PAUL  
; APPLICANT: SMITH, VICTORIA  
; APPLICANT: SPENCER, SUSAN D.  
; APPLICANT: WILLIAMS, P. MICKEY  
; APPLICANT: WU, THOMAS D.  
; APPLICANT: ZHANG, ZEMIN

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND  
TREATMENT OF TUMOR

FILE REFERENCE: P5014E1-PCT  
CURRENT APPLICATION NUMBER: US/10/331,496A  
CURRENT FILING DATE: 2002-12-30  
PRIOR APPLICATION NUMBER: US 60/345,444  
PRIOR FILING DATE: 2002-01-02  
PRIOR APPLICATION NUMBER: US 60/351,885  
PRIOR FILING DATE: 2002-01-25  
PRIOR APPLICATION NUMBER: US 60/360,066  
PRIOR FILING DATE: 2002-02-25  
PRIOR APPLICATION NUMBER: US 60/362,004  
PRIOR FILING DATE: 2002-03-05  
PRIOR APPLICATION NUMBER: US 60/366,869  
PRIOR FILING DATE: 2002-03-20  
PRIOR APPLICATION NUMBER: US 60/366,284  
PRIOR FILING DATE: 2002-03-21  
PRIOR APPLICATION NUMBER: US 60/368,679  
PRIOR FILING DATE: 2002-03-28  
PRIOR APPLICATION NUMBER: US 60/404,809  
PRIOR FILING DATE: 2002-08-19  
PRIOR APPLICATION NUMBER: US 60/405,645  
PRIOR FILING DATE: 2002-08-21  
NUMBER OF SEQ ID NOS: 95  
SEQ ID NO 37  
LENGTH: 129  
TYPE: PRT  
ORGANISM: Homo sapiens

US-10-331-496A-37

Query Match 84.7%; Score 199; DB 15; Length 129;  
Best Local Similarity 84.1%; Pred. No. 1.4e-15;  
Matches 37; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PPAPFLLWPILGGALSLTFVLGSLGFLVWRCRRSSPPPX 44  
DB 71 PPAPFLLWPILGGALSLTFVLGSLGFLVWRCRRREKFTTPI 114

## RESULT 8

US-10-295-027-444  
; Sequence 444, Application US/10295027  
; Publication No. US20030232350A1

GENERAL INFORMATION:

APPLICANT: Afar, Daniel  
APPLICANT: Aziz, Natasha  
APPLICANT: Ginsberg, Wendy M.  
APPLICANT: Gish, Kurt C.  
APPLICANT: Glynn, Richard  
APPLICANT: Hevezi, Peter A.  
APPLICANT: Mack, David H.  
APPLICANT: Murray, Richard  
APPLICANT: Watson, Susan R.  
APPLICANT: Eos Biotechnology, Inc.

TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and  
Methods of Screening for Modulators of Cancer  
FILE REFERENCE: 018501-012500US  
CURRENT APPLICATION NUMBER: US/10/295,027  
CURRENT FILING DATE: 2002-11-13  
PRIOR APPLICATION NUMBER: US 09/663,733

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; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 444
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-444

Query Match      84.7%; Score 199; DB 15; Length 129;
Best Local Similarity 84.1%; Pred. No. 1.4e-15;
Matches 37; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

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Db 71 PPAPFLLPILGGALSITFVLGSLGFLVWRCRRREKFTTPI 114
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RESULT 9
US-10-295-027-1305
; Sequence 1305, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
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; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1305
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-1305

Query Match      84.7%; Score 199; DB 15; Length 129;
Best Local Similarity 84.1%; Pred. No. 1.4e-15;
Matches 37; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

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Db 71 PPAPFLLPILGGALSITFVLGSLGFLVWRCRRREKFTTPI 114
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RESULT 10
US-10-617-217A-178
; Sequence 178, Application US/10617217A
; Publication No. US20040081986A1
; GENERAL INFORMATION:
; APPLICANT: MATSUDA, Akio et al.
; TITLE OF INVENTION: NF-KB ACTIVATING GENE
; FILE REFERENCE: 1254-0229P
; CURRENT APPLICATION NUMBER: US/10/617,217A
; CURRENT FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: JP 2000-402288
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: JP 2001-088912
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: JP 2001-254018
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/258,315
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/278,640
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: US 60/314,385
; PRIOR FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 178
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-617-217A-178

Query Match      84.7%; Score 199; DB 15; Length 129;
Best Local Similarity 84.1%; Pred. No. 1.4e-15;
Matches 37; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

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Db 71 PPAPFLLPILGGALSITFVLGSLGFLVWRCRRREKFTTPI 114
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RESULT 11
US-09-742-454A-5
; Sequence 5, Application US/09742454A
; Patent No. US20020041876A1
; GENERAL INFORMATION:
; APPLICANT: WILEY, Steven R.
; TITLE OF INVENTION: TWEAK Receptor
; FILE REFERENCE: 2968-B
; CURRENT APPLICATION NUMBER: US/09/742,454A
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/172,878
; PRIOR FILING DATE: 1999-12-20
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; PRIOR APPLICATION NUMBER: 60/203,347  
; PRIOR FILING DATE: 2000-05-10  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 129  
; TYPE: PRT  
; ORGANISM: Mus sp.  
US-09-742-454A-5

Query Match 69.8%; Score 164; DB 9; Length 129;  
Best Local Similarity 70.5%; Pred. No. 1.7e-11;  
Matches 31; Conservative 2; Mismatches 11; Indels 0; Gaps 0;  
Qy 1 PPAPRLWPILGGALSITFVLGSLGFLVWRCRRSSPPX 44  
Db 71 PPAHRLWPILGGALSILVILVSSFLVWRCRRREKFTPI 114

RESULT 12  
US-09-883-777-5  
; Sequence 5, Application US/09883777  
; Patent No. US20020110853A1  
; GENERAL INFORMATION:  
; APPLICANT: Wiley, Steven R.  
; TITLE OF INVENTION: TWEAK RECEPTOR  
; FILE REFERENCE: 2968-C  
; CURRENT APPLICATION NUMBER: US/09/883,777  
; CURRENT FILING DATE: 2001-06-18  
; PRIOR APPLICATION NUMBER: US 60/172,878  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: US 60/203,347  
; PRIOR FILING DATE: 2000-05-10  
; PRIOR APPLICATION NUMBER: PCT/US00/34755  
; PRIOR FILING DATE: 2000-12-19  
; PRIOR APPLICATION NUMBER: US 09/742,454  
; PRIOR FILING DATE: 2000-12-19  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 129  
; TYPE: PRT  
; ORGANISM: Mus sp.  
US-09-883-777-5

Query Match 69.8%; Score 164; DB 9; Length 129;  
Best Local Similarity 70.5%; Pred. No. 1.7e-11;  
Matches 31; Conservative 2; Mismatches 11; Indels 0; Gaps 0;  
Qy 1 PPAPRLWPILGGALSITFVLGSLGFLVWRCRRSSPPX 44  
Db 71 PPAHRLWPILGGALSILVILVSSFLVWRCRRREKFTPI 114

RESULT 13  
US-10-257-174-44  
; Sequence 44, Application US/10257174  
; Publication No. US20040034194A1  
; GENERAL INFORMATION:  
; APPLICANT: Agarwal, Pankaj  
; APPLICANT: Murdoch, Paul R.  
; APPLICANT: Rizvi, Safia K.  
; APPLICANT: Smith, Randall F.  
; APPLICANT: Xiang, Zhaoqing  
; TITLE OF INVENTION: NOVEL COMPOUNDS  
; FILE REFERENCE: GP50022  
; CURRENT APPLICATION NUMBER: US/10/257,174  
; CURRENT FILING DATE: 2002-10-10  
; PRIOR APPLICATION NUMBER: PCT/US01/11797  
; PRIOR FILING DATE: 2001-04-11  
; PRIOR APPLICATION NUMBER: 60/196,603  
; PRIOR FILING DATE: 2000-04-13  
; PRIOR APPLICATION NUMBER: 60/199,417

; PRIOR FILING DATE: 2000-04-24  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 44  
; LENGTH: 426  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-257-174-44

Query Match 28.5%; Score 67; DB 15; Length 426;  
Best Local Similarity 40.5%; Pred. No. 11;  
Matches 17; Conservative 5; Mismatches 16; Indels 4; Gaps 2;  
Qy 1 PPAPRLWPILGGALSITFVLGSLGFLVWRCRRSSSP 41  
Db 387 PPAP---VVPILGAVAVLVALSLGLGLLAWRPGCLRALGPG 425

RESULT 14  
US-10-343-357-6  
; Sequence 6, Application US/10343357  
; Publication No. US20040058341A1  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE GENOMICS, INC.; TANG, Y. Tom  
; APPLICANT: ELLIOTT, Vicki S.; RAMKUMAR, Jayalaxmi  
; APPLICANT: YAO, Monique G.; BURFORD, Neil  
; APPLICANT: WANG, Yumei E.; STEWART, Elizabeth A.  
; APPLICANT: GANDHI, Ameena R.; ARVIZU, Chandra S.  
; APPLICANT: LEE, Ernestine A.; HAFALIA, April J.A.  
; APPLICANT: LU, Dyung Alma M.; TRIBOULEY, Catherine M.  
; APPLICANT: GRIFFIN, Jennifer A.; BAUGHN, Mariah R.  
; APPLICANT: YUE, Henry; WARREN, Bridget A.  
; APPLICANT: NGUYEN, Dannel B.; CHAWLA, Narinder K.  
; APPLICANT: KEARNEY, Liam  
; TITLE OF INVENTION: PROTEIN PHOSPHATASES  
; FILE REFERENCE: PI-0173 PCT  
; CURRENT APPLICATION NUMBER: US/10/343,357  
; CURRENT FILING DATE: 2003-01-28  
; PRIOR APPLICATION NUMBER: PCT/US01/23716  
; PRIOR FILING DATE: 2001-07-26  
; PRIOR APPLICATION NUMBER: US 60/221,679  
; PRIOR FILING DATE: 2000-07-28  
; PRIOR APPLICATION NUMBER: US 60/223,272  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: US 60/224,309  
; PRIOR FILING DATE: 2000-08-10  
; PRIOR APPLICATION NUMBER: US 60/226,728  
; PRIOR FILING DATE: 2000-08-18  
; PRIOR APPLICATION NUMBER: US 60/229,254  
; PRIOR FILING DATE: 2000-08-30  
; PRIOR APPLICATION NUMBER: US 60/231,366  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PERL Program  
; SEQ ID NO 6  
; LENGTH: 426  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20040058341A1 7480440CD1  
US-10-343-357-6

Query Match 28.5%; Score 67; DB 15; Length 426;  
Best Local Similarity 40.5%; Pred. No. 11;  
Matches 17; Conservative 5; Mismatches 16; Indels 4; Gaps 2;  
Qy 1 PPAPRLWPILGGALSITFVLGSLGFLVWRCRRSSSP 41  
Db 387 PPAP---VVPILGAVAVLVALSLGLGLLAWRPGCLRALGPG 425

RESULT 15

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US-10-282-122A-48721
; Sequence 48721, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48721
; LENGTH: 742
; TYPE: PRT
; ORGANISM: Bacteroides fragilis
US-10-282-122A-48721

Query Match      27.4%; Score 64.5; DB 15; Length 742;
Best Local Similarity 40.9%; Pred. No. 38;
Matches 18; Conservative 7; Mismatches 8; Indels 11; Gaps 3;

Qy 4 PFRLWPI-----LGGALSTFVLGLSG--FLVWRECRERS 39
||: ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 337 PEKTRHPVWVFWFALIG---SITAIVSLISGITYLYWRETKRKS 377

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Search completed: February 14, 2005, 07:35:50  
Job time : 131 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 14, 2005, 07:15:17 ; Search time 43 Seconds  
(without alignments)

76.385 Million cell updates/sec

Title: US-10-062-831-59\_COPY\_71\_114

Perfect score: 235

Sequence: 1 PPAPFRLWLPILGGALSLTF.....LSGFLVWRCRRRSSPPPX 44

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Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents\_AA\*

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2: /cgm2\_6/ptodata/1/iaa/5B\_COMB.pep:\*  
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4: /cgm2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
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6: /cgm2\_6/ptodata/1/iaa/backfiles.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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1	235	100.0	114	4	US-09-690-454-59
2	199	84.7	129	4	US-09-883-777-4
3	199	84.7	129	4	US-09-949-016-6914
4	199	84.7	129	4	US-09-742-454A-4
5	164	69.8	129	4	US-09-883-777-5
6	164	69.8	129	4	US-09-742-454A-5
7	63	26.8	365	4	US-09-949-016-6907
8	63	26.8	391	4	US-09-949-016-7325
9	61	26.0	992	1	US-08-127-499A-1
10	61	26.0	992	1	US-08-482-847-1
11	60	25.5	309	4	US-09-883-777-7
12	60	25.5	309	4	US-09-742-454A-7
13	60	25.5	730	1	US-08-121-713D-58
14	60	25.5	730	1	US-08-835-268-58
15	60	25.5	730	1	US-09-060-692-58
16	60	25.5	730	3	US-08-833-391-58
17	60	25.5	730	3	US-09-060-610-58
18	60	25.5	730	5	PCT-US94-10151A-58
19	60	25.5	839	4	US-09-489-039A-13252
20	59.5	25.3	137	4	US-09-489-039A-11239
21	58.5	24.9	153	4	US-09-252-991A-18571
22	58.5	24.9	231	4	US-09-724-623-116
23	58.5	24.9	617	4	US-09-252-991A-29507
24	58	24.7	153	4	US-09-452-937A-30
25	57.5	24.5	256	4	US-09-071-035-300
26	57.5	24.5	284	4	US-09-071-035-298
27	57.5	24.5	284	4	US-09-933-999A-6

28	57.5	24.5	315	4	US-09-134-000C-6125	Sequence 6125, Ap
29	57.5	24.5	1006	4	US-09-949-016-7897	Sequence 7897, Ap
30	57.5	24.5	1445	1	US-08-015-986A-2	Sequence 2, Appli
31	57.5	24.5	1445	2	US-08-446-363-2	Sequence 2, Appli
32	57	24.3	153	4	US-08-252-991A-31363	Sequence 31363, A
33	57	24.3	652	2	US-08-751-305-2	Sequence 2, Appli
34	56	23.8	197	4	US-09-252-991A-30359	Sequence 30359, A
35	56	23.8	278	3	US-08-663-082-4	Sequence 4, Appli
36	56	23.8	402	4	US-09-252-991A-18195	Sequence 18195, A
37	56	23.8	403	4	US-09-252-991A-30953	Sequence 30953, A
38	56	23.8	483	4	US-09-543-681A-5752	Sequence 5752, Ap
39	56	23.8	488	4	US-09-949-016-9120	Sequence 9120, Ap
40	56	23.8	851	1	US-08-369-796-2	Sequence 2, Appli
41	56	23.8	851	2	US-08-852-091-2	Sequence 2, Appli
42	56	23.8	851	2	US-08-820-754-2	Sequence 2, Appli
43	56	23.8	851	3	US-08-956-652-2	Sequence 2, Appli
44	56	23.8	851	3	US-08-956-652-2	Sequence 2, Appli
45	56	23.8	851	3	US-09-012-710-2	Sequence 2, Appli

## ALIGNMENTS

### RESULT 1

US-09-690-454-59  
; Sequence 59, Application US/09690454  
; Patent No. 6531447  
; GENERAL INFORMATION:  
; APPLICANT: Steven M. Ruben, et al.  
; TITLE OF INVENTION: 32 Human Secreted Proteins  
; FILE REFERENCE: PZ006P1  
; CURRENT APPLICATION NUMBER: US/09/690,454  
; CURRENT FILING DATE: 2000-10-18  
; PRIOR APPLICATION NUMBER: 09/189,144  
; PRIOR FILING DATE: 1998-11-10  
; PRIOR APPLICATION NUMBER: 60/044,039  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/048,093  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/048,190  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/050,935  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/048,101  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/048,356  
; PRIOR FILING DATE: May 30, 1997  
; PRIOR APPLICATION NUMBER: 60/056,250  
; PRIOR FILING DATE: August 29, 1997  
; PRIOR APPLICATION NUMBER: 60/056,296  
; PRIOR FILING DATE: August 29, 1997  
; PRIOR APPLICATION NUMBER: 60/056,293  
; PRIOR FILING DATE: August 29, 1997  
; NUMBER OF SEQ ID NOS: 229  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 59  
; LENGTH: 114  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (114)  
; OTHER INFORMATION: Xaa equals stop translation  
US-09-690-454-59

Query Match 100.0%; Score 235; DB 4; Length 114;  
Best Local Similarity 100.0%; Pred. No. 8.1e-24;  
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 PPAPFRLWLPILGGALSLTFVLGSLGFLVWRCRRRSSPPPX 44

Db 71 PPAPFRLWLPILGGALSLTFVLGSLGFLVWRCRRRSSPPPX 114

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RESULT 2
US-09-883-777-4
; Sequence 4, Application US/09883777
; Patent No. 6727225
; GENERAL INFORMATION:
; APPLICANT: WILEY, Steven R.
; TITLE OF INVENTION: TWEAK RECEPTOR
; FILE REFERENCE: 2968-C
; CURRENT APPLICATION NUMBER: US/09/883,777
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: US 60/203,347
; PRIOR FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: PCT/US00/34755
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/742,454
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 129
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-883-777-4

Query Match      84.7%; Score 199; DB 4; Length 129;
Best Local Similarity 84.1%; Pred. No. 5.6e-19;
Matches 37; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PPAPRLLWPILGGALSLTFVLGSLGFLVWRCRRRSSPPPX 44
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DB 71 PPAPRLLWPILGGALSLTFVLGSLGFLVWRCRRRKFTTPI 114

RESULT 3
US-09-949-016-6914
; Sequence 6914, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6914
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6914

Query Match      84.7%; Score 199; DB 4; Length 129;
Best Local Similarity 84.1%; Pred. No. 5.6e-19;
Matches 37; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PPAPRLLWPILGGALSLTFVLGSLGFLVWRCRRRSSPPPX 44
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DB 71 PPAPRLLWPILGGALSLTFVLGSLGFLVWRCRRRKFTTPI 114

RESULT 4
US-09-742-454A-4
; Sequence 4, Application US/09742454A
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; Patent No. 6824773
; GENERAL INFORMATION:
; APPLICANT: WILEY, Steven R.
; TITLE OF INVENTION: TWEAK RECEPTOR
; FILE REFERENCE: 2968-B
; CURRENT APPLICATION NUMBER: US/09/742,454A
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: 60/203,347
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-742-454A-4

Query Match      84.7%; Score 199; DB 4; Length 129;
Best Local Similarity 84.1%; Pred. No. 5.6e-19;
Matches 37; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 PPAPRLLWPILGGALSLTFVLGSLGFLVWRCRRRSSPPPX 44
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DB 71 PPAPRLLWPILGGALSLTFVLGSLGFLVWRCRRRKFTTPI 114

RESULT 5
US-09-883-777-5
; Sequence 5, Application US/09883777
; Patent No. 6727225
; GENERAL INFORMATION:
; APPLICANT: WILEY, Steven R.
; TITLE OF INVENTION: TWEAK RECEPTOR
; FILE REFERENCE: 2968-C
; CURRENT APPLICATION NUMBER: US/09/883,777
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US 60/172,878
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: US 60/203,347
; PRIOR FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: PCT/US00/34755
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: US 09/742,454
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-883-777-5

Query Match      69.8%; Score 164; DB 4; Length 129;
Best Local Similarity 70.5%; Pred. No. 2.5e-14;
Matches 31; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

QY 1 PPAPRLLWPILGGALSLTFVLGSLGFLVWRCRRRSSPPPX 44
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DB 71 PPAHFRLLWPILGGALSLVLVLAIVSSFLVWRCRRRKFTTPI 114

RESULT 6
US-09-742-454A-5
; Sequence 5, Application US/09742454A
; Patent No. 6824773
; GENERAL INFORMATION:
; APPLICANT: WILEY, Steven R.
; TITLE OF INVENTION: TWEAK RECEPTOR
; FILE REFERENCE: 2968-B
; CURRENT APPLICATION NUMBER: US/09/742,454A
; CURRENT FILING DATE: 2000-12-19
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; PRIOR APPLICATION NUMBER: 60/172,878  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: 60/203,347  
; PRIOR FILING DATE: 2000-05-10  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 129  
; TYPE: PRT  
; ORGANISM: Mus sp.  
US-09-742-454A-5

Query Match 69.8%; Score 164; DB 4; Length 129;  
Best Local Similarity 70.5%; Pred. No. 2.5e-14;  
Matches 31; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

Qy 1 PPAPRLWPILGGALSLTFVLGSLGFLVWRCRRSSPPPX 44  
Db 71 PPAPRLWPILGGALSLVLVLSFLVWRCRRRKKFTTPI 114

## RESULT 7

US-09-949-016-6907  
; Sequence 6907, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6907  
; LENGTH: 365  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-6907

Query Match 26.8%; Score 63; DB 4; Length 365;  
Best Local Similarity 45.9%; Pred. No. 2.1;  
Matches 17; Conservative 5; Mismatches 13; Indels 2; Gaps 2;

Qy 5 PRLWPILGGALSLT-FVLGSLGFLVWRCRRSS 40  
Db 220 FR-FWPLVIVILSALFLGTACFCVWRRRKKQKS 255

## RESULT 8

US-09-949-016-7325  
; Sequence 7325, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7325  
; LENGTH: 391  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-7325

Query Match 26.8%; Score 63; DB 4; Length 391;  
Best Local Similarity 45.9%; Pred. No. 2.2;  
Matches 17; Conservative 5; Mismatches 13; Indels 2; Gaps 2;

Qy 5 PRLWPILGGALSLT-FVLGSLGFLVWRCRRSS 40  
Db 246 FR-FWPLVIVILSALFLGTACFCVWRRRKKQKS 281

## RESULT 9

US-08-127-499A-1  
; Sequence 1, Application US/08127499A  
; Patent No. 5510264  
; GENERAL INFORMATION:  
; APPLICANT: VAN ALSTYNE, Diane  
; APPLICANT: SHARMA, Lawrence Rajendra  
; TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED  
; TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES  
; NUMBER OF SEQUENCES: 40  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/127,499A  
; FILING DATE: 28-SEP-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BENT, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 51916/102/INBI  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 992 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
US-08-127-499A-1

Query Match 26.0%; Score 61; DB 1; Length 992;  
Best Local Similarity 38.8%; Pred. No. 12;  
Matches 19; Conservative 6; Mismatches 16; Indels 8; Gaps 3;

Qy 3 APFRLWPILGGALSL-----TFVLGSLGFLVWRCRR--ERSPPPX 44  
Db 518 SPASALMLATANALSLDHAFAFVL-LVPWVLIFWVCRCRACRRAPPPP 565

## RESULT 10

US-08-482-847-1  
; Sequence 1, Application US/08482847  
; Patent No. 5556757  
; GENERAL INFORMATION:  
; APPLICANT: VAN ALSTYNE, Diane  
; APPLICANT: SHARMA, Lawrence Rajendra

;; TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR  
;; TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR  
;; TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF  
;; NUMBER OF SEQUENCES: 40  
;; CORRESPONDENCE ADDRESSES:  
;; ADDRESSEE: Foley & Lardner  
;; STREET: 3000 K Street, N.W., Suite 500  
;; CITY: Washington  
;; STATE: D.C.  
;; COUNTRY: USA  
;; ZIP: 20007-5109  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/482,847  
;; FILING DATE: 07-JUN-1995  
;; CLASSIFICATION: 514  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/127,499  
;; FILING DATE: 28-SEP-1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: BENT, Stephen A.  
;; REGISTRATION NUMBER: 29,768  
;; REFERENCE/DOCKET NUMBER: 51916/104/INBI  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (202)672-5300  
;; TELEFAX: (202)672-5399  
;; TELEX: 904136  
;; INFORMATION FOR SEQ ID NO: 1:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 992 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS:  
;; TOPOLOGY: unknown  
US-08-482-847-1

Query Match 26.0%; Score 61; DB 1; Length 992;  
Best Local Similarity 38.8%; Pred. No. 12;  
Matches 19; Conservative 6; Mismatches 16; Indels 8; Gaps 3;  
Qy 3 APFRLWPILGALSL-----TFVLGILSGFLVWRCRR--ERSPPPX 44  
Db 518 SPASALWLANALSLDRAFAFVL-LVPMVLIFWVCRRCRRPAPPP 565

RESULT 11  
US-09-883-777-7  
; Sequence 7, Application US/09883777  
; Patent No. 6727225  
; GENERAL INFORMATION:  
; APPLICANT: Wiley, Steven R.  
; TITLE OF INVENTION: TWEAK RECEPTOR  
; FILE REFERENCE: 2968-C  
; CURRENT APPLICATION NUMBER: US/09/883,777  
; PRIOR FILING DATE: 2001-05-18  
; PRIOR APPLICATION NUMBER: US 60/172,878  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: US 60/203,347  
; PRIOR FILING DATE: 2000-05-10  
; PRIOR APPLICATION NUMBER: PC/US00/34755  
; PRIOR FILING DATE: 2000-12-19  
; PRIOR APPLICATION NUMBER: US 09/742,454  
; PRIOR FILING DATE: 2000-12-19  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7  
; LENGTH: 309  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:

;; OTHER INFORMATION: Human TWEAK receptor fusion protein construct  
US-09-883-777-7  
Query Match 25.5%; Score 60; DB 4; Length 309;  
Best Local Similarity 31.0%; Pred. No. 4.3;  
Matches 13; Conservative 2; Mismatches 5; Indels 22; Gaps 1;  
Qy 1 PPAPFRLWPILGALSLTFVLGILSGFLVWRCRRRSRSP 42  
Db 71 PPAPFRL-----WRSCDKTHTCPP 90

RESULT 12  
US-09-742-454A-7  
; Sequence 7, Application US/09742454A  
; Patent No. 6824773  
; GENERAL INFORMATION:  
; APPLICANT: WILEY, Steven R.  
; TITLE OF INVENTION: TWEAK Receptor  
; FILE REFERENCE: 2968-B  
; CURRENT APPLICATION NUMBER: US/09/742,454A  
; PRIOR FILING DATE: 2000-12-19  
; PRIOR APPLICATION NUMBER: 60/172,878  
; PRIOR FILING DATE: 1999-12-20  
; PRIOR APPLICATION NUMBER: 60/203,347  
; PRIOR FILING DATE: 2000-05-10  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 309  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: human TWEAK  
; OTHER INFORMATION: receptor fusion protein construct  
US-09-742-454A-7

Query Match 25.5%; Score 60; DB 4; Length 309;  
Best Local Similarity 31.0%; Pred. No. 4.3;  
Matches 13; Conservative 2; Mismatches 5; Indels 22; Gaps 1;  
Qy 1 PPAPFRLWPILGALSLTFVLGILSGFLVWRCRRRSRSP 42  
Db 71 PPAPFRL-----WRSCDKTHTCPP 90

RESULT 13  
US-08-121-713D-58  
; Sequence 58, Application US/08121713D  
; Patent No. 5639856  
; GENERAL INFORMATION:  
; APPLICANT: Goodman, Corey S.  
; APPLICANT: Kolodkin, Alex L.  
; APPLICANT: Matthes, David  
; APPLICANT: Bentley, David R.  
; APPLICANT: O'Connor, Timothy  
; TITLE OF INVENTION: The Semaphorin Gene Family  
; NUMBER OF SEQUENCES: 100  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
; STREET: 268 Bush Street, Suite 3200  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/121,713D  
; FILING DATE: 13-SEP-1993

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; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B94-002-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)343-4341
; TELEFAX: (415) 343-4342
; TELEX:
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 730 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-121-713D-58

Query Match 25.5%; Score 60; DB 1; Length 730;
Best Local Similarity 48.4%; Pred. No. 11;
Matches 15; Conservative 4; Mismatches 8; Indels 4; Gaps 1;

QY 14 GALSITFVLGSLGVWRCRRSSPPX 44
DB 639 GAL----VVGFIGFLFSRRCRGEDYDMPF 665

RESULT 14
US-08-835-268-58
; Sequence 58, Application US/08835268
; Patent No. 5807826
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey S.
; APPLICANT: Kolodkin, Alex L.
; APPLICANT: Matthes, David
; APPLICANT: Bentley, David R.
; APPLICANT: O'Connor, Timothy
; TITLE OF INVENTION: The Semaphorin Gene Family
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/835,268
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,713
; FILING DATE: 13-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B94-002-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)343-4341
; TELEFAX: (415) 343-4342
; TELEX:
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 730 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-835-268-58

Search completed: February 14, 2005, 07:24:52
Job time : 44 secs

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Query Match 25.5%; Score 60; DB 1; Length 730;
Best Local Similarity 48.4%; Pred. No. 11;
Matches 15; Conservative 4; Mismatches 8; Indels 4; Gaps 1;

QY 14 GALSITFVLGSLGVWRCRRSSPPX 44
DB 639 GAL----VVGFIGFLFSRRCRGEDYDMPF 665

RESULT 15
US-09-060-692-58
; Sequence 58, Application US/09060692
; Patent No. 5935865
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey S.
; APPLICANT: Kolodkin, Alex L.
; APPLICANT: Matthes, David
; APPLICANT: Bentley, David R.
; APPLICANT: O'Connor, Timothy
; TITLE OF INVENTION: The Semaphorin Gene Family
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/060,692
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,713
; FILING DATE: 13-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B94-002-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)343-4341
; TELEFAX: (415) 343-4342
; TELEX:
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 730 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-060-692-58

Query Match 25.5%; Score 60; DB 2; Length 730;
Best Local Similarity 48.4%; Pred. No. 11;
Matches 15; Conservative 4; Mismatches 8; Indels 4; Gaps 1;

QY 14 GALSITFVLGSLGVWRCRRSSPPX 44
DB 639 GAL----VVGFIGFLFSRRCRGEDYDMPF 665

Search completed: February 14, 2005, 07:24:52
Job time : 44 secs

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